



A13

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<120> CLASP-3 Transmembrane Protein

<130> 020054-000311US

<140> US 09/737,246

<141> 2000-12-13

<150> US 60/160,860

<151> 1999-10-21

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<170> PatentIn Ver. 2.1

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1915 1920 1925 1930	
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Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His Gly Glu	
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Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser His Ala	
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Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys Lys Thr	
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Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro Lys Met	
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Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp Pro	
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Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe	
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Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly	
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Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile Arg Ser	
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cac ccc agt gcc tcc ctt tac cta cta atg agg caa aac ttt gag att	2065
His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile	
675 680 685	
ggg aat aac ttt gcc agg gtt aaa atg cag gta cca atg tca cta tcc	2113
Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser Leu Ser	
690 695 700	
tcc ttg gtg ggc aca tct cag aat ttt aat gaa gaa ttc tta aga cgt	2161
Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu Arg Arg	
705 710 715 720	
tct cta aag act ata ttg aca tat gct gaa gaa gat ctg gaa ttg agg	2209
Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu Leu Arg	
725 730 735	
gaa aca aca ttt cct gat cag gtc cag gat ctg gtt ttc aat ctc cat	2257
Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn Leu His	
740 745 750	
atg att ctt tct gat act gtg aaa atg aag gaa cac cag gag gat cct	2305
Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu Asp Pro	
755 760 765	
gaa atg ttg att gat cta atg tac aga att gcc aag ggt tac cag acc	2353
Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr Gln Thr	
770 775 780	
tct cca gat ctg cga ttg acc tgg ttg cag aac atg gca ggc aag cac	2401
Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His	
785 790 795 800	
tca gaa cga agc aat cat gct gaa gct gca cag tgt cta gtc cac tca	2449
Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val His Ser	
805 810 815	

gca gca ctt gtt gct gaa tat ttg agc atg ctg gag gac cgg aaa tat	2497
Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg Lys Tyr	
820 825 830	
ctt cct gtg gga tgt gta aca ttt cag aat att tca tct aat gtt tta	2545
Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn Val Leu	
835 840 845	
gaa gaa tct gcg gtc tca gat gat gtg gta tct cca gat gaa gaa ggt	2593
Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu Glu Gly	
850 855 860	
atc tgc tct gga aaa tac ttt act gag tca gga ctt gtg gga tta ctg	2641
Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu	
865 870 875 880	
gaa caa gca gct gct tcc ttc tct atg gct ggc atg tat gaa gca gtt	2689
Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu Ala Val	
885 890 895	
aat gaa gtt tac aaa gta ctt att cct att cat gaa gct aat cgg gat	2737
Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn Arg Asp	
900 905 910	
gca aag aaa cta tcc aca att cat ggt aaa ctt caa gaa gca ttc agc	2785
Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala Phe Ser	
915 920 925	
aaa att gtt cat cag agt act ggc tgg gag cgg atg ttt ggc acc tat	2833
Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr	
930 935 940	
ttt cgt gtt ggt ttt tat gga acc aag ttc ggg gat ttg gat gaa caa	2881
Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln	
945 950 955 960	
gaa ttt gtt tac aag gag cct gca ata acc aaa ctt gca gag ata tct	2929
Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser	
965 970 975	
cac aga ttg gag gga ttt tac gga gaa aga ttt gga gag gat gtg gtt	2977
His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val	
980 985 990	
gaa gta atc aaa gac tct aat cct gta gac aag tgt aaa tta gat cct	3025
Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro	
995 1000 1005	
aac aag gca tat att cag att acc tat gtg gag cca tac ttt gac aca	3073
Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr	
1010 1015 1020	
tat gag atg aag gac aga atc acc tat ttc gac aaa aat tac aat ctt	3121
Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu	
1025 1030 1035 1040	
cgt cga ttc atg tac tgt aca ccc ttt act tta gat ggc cgt gcc cat	3169
Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His	
1045 1050 1055	

ggg gaa ctt cat gaa caa ttc aaa agg aag acc att ctg act acg tct	3217
Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser	
1060 1065 1070	
cat gcc ttt cct tat att aaa aca agg gtc aat gtc act cat aaa gaa	3265
His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu	
1075 1080 1085	
gag atc atc tta aca cca att gaa gtt gct att gag gac atg cag aaa	3313
Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys	
1090 1095 1100	
aag aca cag gag ttg gca ttt gca aca cat cag gat ccc gca gac ccc	3361
Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro	
1105 1110 1115 1120	
aaa atg ctt cag atg gta ctc cag gga tct gta ggc acc aca gtg aat	3409
Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn	
1125 1130 1135	
cag ggg cct ttg gaa gtt gcc cag gtt ttt ctg tct gaa ata cct agt	3457
Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser	
1140 1145 1150	
gac cca aag ctc ttc aga cat cat aat aaa ctg cga ctc tgc ttt aaa	3505
Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys	
1155 1160 1165	
gat ttt act aaa agg tgt gaa gat gcc tta aga aaa aat aag agc tta	3553
Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu	
1170 1175 1180	
att ggg ccg gtt caa aag gag tat caa agg gaa ttg ggg aaa cta tct	3601
Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser	
1185 1190 1195 1200	
tcg cct taa agaggcccta cagccctaga tcacagaaag tccctcagtt	3650
Ser Pro	
atccaagcca gtattgcttg tcccctgccca cagagattcc ttcagtcgaa tgagctttcg	3710
caaaatggat ctctaaactg aatgcacttg ttttattcat ctgcaaagag ccatgtattc	3770
aacatcgagt gtgaaaagat ctattggaaa ccaacatgga atggaattct ggaaattatt	3830
attcattgaa gaatgcagtg gccaaagaaa tatcaaagt agattgttaa cgcttgagaa	3890
tcatggctat ggtttctaatt gttcgggtaa caagctgtta tcttttaaga cattttaatg	3950
actcaaaggt aactataca ttaccatta ttataccat agctaagggt aaaaatttat	4010
tcactttaag ttcgtatttt ttaatttata tcaccattta tagattcatt ttggacccat	4070
tttaaagtga gtaatgctta ttttaaagggt actaaaaaat atgtgaatgt ttacctcgtg	4130
cgcgccaggg cctc	4144

<210> 8
 <211> 1202
 <212> PRT
 <213> Homo sapiens
 <223> preliminary CLASP-3

<400> 8

Arg	Val	Asn	Arg	Ser	Arg	Ser	Leu	Ser	Asn	Ser	Asn	Pro	Asp	Ile	Ser	1	5	10	15
Gly	Thr	Pro	Thr	Ser	Pro	Asp	Asp	Glu	Val	Arg	Ser	Ile	Ile	Gly	Ser	20	25	30	
Lys	Gly	Leu	Asp	Arg	Ser	Asn	Ser	Trp	Val	Asn	Thr	Gly	Gly	Pro	Lys	35	40	45	
Ala	Ala	Pro	Trp	Gly	Ser	Asn	Pro	Ser	Pro	Ser	Ala	Glu	Ser	Thr	Gln	50	55	60	
Ala	Met	Asp	Arg	Ser	Cys	Asn	Arg	Met	Ser	Ser	His	Thr	Glu	Thr	Ser	65	70	75	80
Ser	Phe	Leu	Gln	Thr	Leu	Thr	Gly	Arg	Leu	Pro	Thr	Lys	Lys	Leu	Phe	85	90	95	
His	Glu	Glu	Leu	Ala	Leu	Gln	Trp	Val	Val	Cys	Ser	Gly	Ser	Val	Arg	100	105	110	
Glu	Ser	Ala	Leu	Gln	Gln	Ala	Trp	Phe	Phe	Phe	Glu	Leu	Met	Val	Lys	115	120	125	
Ser	Met	Val	His	His	Leu	Tyr	Phe	Asn	Asp	Lys	Leu	Glu	Ala	Pro	Arg	130	135	140	
Lys	Ser	Arg	Phe	Pro	Glu	Arg	Phe	Met	Asp	Asp	Ile	Ala	Ala	Leu	Val	145	150	155	160
Ser	Thr	Ile	Ala	Ser	Asp	Ile	Val	Ser	Arg	Phe	Gln	Lys	Asp	Thr	Glu	165	170	175	
Met	Val	Glu	Arg	Leu	Asn	Thr	Ser	Leu	Ala	Phe	Phe	Leu	Asn	Asp	Leu	180	185	190	
Leu	Ser	Val	Met	Asp	Arg	Gly	Phe	Val	Phe	Ser	Leu	Ile	Lys	Ser	Cys	195	200	205	
Tyr	Lys	Gln	Val	Ser	Ser	Lys	Leu	Tyr	Ser	Leu	Pro	Asn	Pro	Ser	Val	210	215	220	
Leu	Val	Ser	Leu	Arg	Leu	Asp	Phe	Leu	Arg	Ile	Ile	Cys	Ser	His	Glu	225	230	235	240
His	Tyr	Val	Thr	Leu	Asn	Leu	Pro	Cys	Ser	Leu	Leu	Thr	Pro	Pro	Ala	245	250	255	
Ser	Pro	Ser	Pro	Ser	Val	Ser	Ser	Ala	Thr	Ser	Gln	Ser	Ser	Gly	Phe	260	265	270	
Ser	Thr	Asn	Val	Gln	Asp	Gln	Lys	Ile	Ala	Asn	Met	Phe	Glu	Leu	Ser	275	280	285	

Val	Pro	Phe	Arg	Gln	Gln	His	Tyr	Leu	Ala	Gly	Leu	Val	Leu	Thr	Glu	290	295	300	
Leu	Ala	Val	Ile	Leu	Asp	Pro	Asp	Ala	Glu	Gly	Leu	Phe	Gly	Leu	His	305	310	315	320
Lys	Lys	Val	Ile	Asn	Met	Val	His	Asn	Leu	Leu	Ser	Ser	His	Asp	Ser	325	330	335	
Asp	Pro	Arg	Tyr	Ser	Asp	Pro	Gln	Ile	Lys	Ala	Arg	Val	Ala	Met	Leu	340	345	350	
Tyr	Leu	Pro	Leu	Ile	Gly	Ile	Ile	Met	Glu	Thr	Val	Pro	Gln	Leu	Tyr	355	360	365	
Asp	Phe	Thr	Glu	Thr	His	Asn	Gln	Arg	Gly	Arg	Pro	Ile	Cys	Ile	Ala	370	375	380	
Thr	Asp	Asp	Tyr	Glu	Ser	Glu	Ser	Gly	Ser	Met	Ile	Ser	Gln	Thr	Val	385	390	395	400
Ala	Met	Ala	Ile	Ala	Gly	Thr	Ser	Val	Pro	Gln	Leu	Thr	Arg	Pro	Gly	405	410	415	
Ser	Phe	Leu	Leu	Thr	Ser	Thr	Ser	Gly	Arg	Gln	His	Thr	Thr	Phe	Ser	420	425	430	
Ala	Glu	Ser	Ser	Arg	Ser	Leu	Leu	Ile	Cys	Leu	Leu	Trp	Val	Leu	Lys	435	440	445	
Asn	Ala	Asp	Glu	Thr	Val	Leu	Gln	Lys	Trp	Phe	Thr	Asp	Leu	Ser	Val	450	455	460	
Leu	Gln	Leu	Asn	Arg	Leu	Leu	Asp	Leu	Leu	Tyr	Leu	Cys	Val	Ser	Cys	465	470	475	480
Phe	Glu	Tyr	Lys	Gly	Lys	Lys	Val	Phe	Glu	Arg	Met	Asn	Ser	Leu	Thr	485	490	495	
Phe	Lys	Lys	Ser	Lys	Asp	Met	Arg	Ala	Lys	Leu	Glu	Glu	Ala	Ile	Leu	500	505	510	
Gly	Ser	Ile	Gly	Ala	Arg	Gln	Glu	Met	Val	Arg	Arg	Ser	Arg	Gly	Gln	515	520	525	
Leu	Glu	Arg	Ser	Pro	Ser	Gly	Ser	Ala	Phe	Gly	Ser	Gln	Glu	Asn	Leu	530	535	540	
Arg	Trp	Arg	Lys	Asp	Met	Thr	His	Trp	Arg	Gln	Asn	Thr	Glu	Lys	Leu	545	550	555	560
Asp	Lys	Ser	Arg	Ala	Glu	Ile	Glu	His	Glu	Ala	Leu	Ile	Asp	Gly	Asn	565	570	575	
Leu	Ala	Thr	Glu	Ala	Asn	Leu	Ile	Ile	Leu	Asp	Thr	Leu	Glu	Ile	Val	580	585	590	
Val	Gln	Thr	Val	Ser	Val	Thr	Glu	Ser	Lys	Glu	Ser	Ile	Leu	Gly	Gly	595	600	605	

Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser Ala Val
610 615 620
Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser Lys Phe
625 630 635 640
Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp Leu Cys
645 650 655
Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile Arg Ser
660 665 670
His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile
675 680 685
Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser Leu Ser
690 695 700
Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu Arg Arg
705 710 715 720
Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu Leu Arg
725 730 735
Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn Leu His
740 745 750
Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu Asp Pro
755 760 765
Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr Gln Thr
770 775 780
Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His
785 790 795 800
Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val His Ser
805 810 815
Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg Lys Tyr
820 825 830
Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn Val Leu
835 840 845
Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu Glu Gly
850 855 860
Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
865 870 875 880
Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu Ala Val
885 890 895
Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn Arg Asp
900 905 910
Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala Phe Ser
915 920 925

Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly Thr Tyr
 930 935 940
 Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
 945 950 955 960
 Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser
 965 970 975
 His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp Val Val
 980 985 990
 Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu Asp Pro
 995 1000 1005
 Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr
 1010 1015 1020
 Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr Asn Leu
 1025 1030 1035 1040
 Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg Ala His
 1045 1050 1055
 Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr Thr Ser
 1060 1065 1070
 His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His Lys Glu
 1075 1080 1085
 Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Gln Lys
 1090 1095 1100
 Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala Asp Pro
 1105 1110 1115 1120
 Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn
 1125 1130 1135
 Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser
 1140 1145 1150
 Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys
 1155 1160 1165
 Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys Ser Leu
 1170 1175 1180
 Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys Leu Ser
 1185 1190 1195 1200
 Ser Pro

<210> 9

<211> 1352

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-2

<400> 9

Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	
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Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu	Leu	Leu	Thr	Phe	
			20					25					30			
Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	Thr	Lys	Lys	Arg	
		35					40					45				
Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	Pro	Leu	Leu	Lys	
	50					55					60					
Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro	Val	Ser	Ala	Asn	
65					70					75					80	
Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu	Gly	Met	Gly	Arg	His	
			85						90					95		
Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys	Pro	Leu	Leu	Lys	
			100					105					110			
Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln	Asp	Gln	His	Leu	
		115					120					125				
His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser	Gly	Ala	Gln	Ala	
	130					135					140					
Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu	His	Ala	Met	Glu	
145					150					155					160	
Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu	Asn	Gln	Leu	Phe	
			165						170					175		
Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala	Val	Asn	Val	Thr	
			180					185					190			
Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu	Glu	Gly	Leu	Glu	
		195					200					205				
Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys	Ala	Glu	Pro	Tyr	
	210					215					220					
Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu	Thr	Lys	Ser	Met	
225					230					235					240	
Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr	Ser	Asn	Lys	Leu	
			245						250					255		
Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile	Lys	Ser	Met	Ala	
			260					265					270			
Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	Arg	Asn	Gln	Arg	
		275					280					285				
Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	Val	Asn	Met	Leu	
	290					295					300					
Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	Glu	Ala	Ser	Lys	
305					310					315					320	

Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	Cys	Phe	Thr	Phe	325	330	335
Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	Tyr	Ile	Ser	Cys	340	345	350
Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	Lys	Phe	Glu	Phe	355	360	365
Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	370	375	380
Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	Asp	Leu	Gln	Leu	385	390	400
Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	Phe	Leu	Val	Gly	405	410	415
Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	Phe	Arg	Glu	Val	420	425	430
Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	Ile	Lys	His	Ser	435	440	445
Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	Arg	Ile	Ala	Thr	450	455	460
Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	Val	Gln	Arg	Ile	465	470	475
Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	Gly	Met	Thr	Val	485	490	495
Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	Leu	Val	Thr	Pro	500	505	510
Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	Asp	Leu	Leu	Gly	515	520	525
Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	Thr	Pro	Asn	Ile	530	535	540
Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	Leu	Ile	Ser	Thr	Asp	545	550	555
Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	Lys	Ser	Asn	Ser	Leu	565	570	575
Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	Ser	Val	Val	Arg	Cys	580	585	590
Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	Leu	Met	Cys	Phe	Leu	595	600	605
Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	Phe	Thr	Tyr	Trp	Asn	610	615	620
Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	Thr	Ile	Ser	Glu	Val	625	630	635

Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn
 645 650 655
 Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu
 660 665 670
 Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu Gln Gln
 675 680 685
 Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His
 690 695 700
 Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala
 705 710 715 720
 Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu
 725 730 735
 Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met
 740 745 750
 Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser
 755 760 765
 Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr
 770 775 780
 Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala
 785 790 795 800
 Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile
 805 810 815
 Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe
 820 825 830
 Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile
 835 840 845
 Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr
 850 855 860
 Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp
 865 870 875 880
 Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr
 885 890 895
 Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His
 900 905 910
 Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys
 915 920 925
 Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met
 930 935 940
 Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys
 945 950 955 960

Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly
 965 970 975
 Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile
 980 985 990
 Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His
 995 1000 1005
 Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly
 1010 1015 1020
 Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu
 1025 1030 1035 1040
 Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp
 1045 1050 1055
 Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu
 1060 1065 1070
 Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu
 1075 1080 1085
 Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu
 1090 1095 1100
 Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe
 1105 1110 1115 1120
 Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His
 1125 1130 1135
 Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys
 1140 1145 1150
 Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr
 1155 1160 1165
 Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr
 1170 1175 1180
 Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met
 1185 1190 1195 1200
 Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val
 1205 1210 1215
 Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln
 1220 1225 1230
 Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr
 1235 1240 1245
 Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val
 1250 1255 1260
 Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu
 1265 1270 1275 1280

Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala
1285 1290 1295

Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln
1300 1305 1310

Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His
1315 1320 1325

Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly
1330 1335 1340

Met Thr Ser Ser Ser Ser Val Val
1345 1350

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<212> PRT
<213> Homo sapiens

<220>
<223> KIAA1058

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Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
20 25 30

Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
35 40 45

Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
50 55 60

Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
65 70 75 80

Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
85 90 95

His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
100 105 110

Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
115 120 125

Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
130 135 140

Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
145 150 155 160

Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
165 170 175

Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
180 185 190

Leu	Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	195	200	205
Ser	Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	210	215	220
Leu	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	225	230	235
Pro	Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Tyr	Leu	Gly	Tyr	Gln	Glu	Leu	245	250	255
Gly	Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	260	265	270
Lys	Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	275	280	285
Gln	Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	290	295	300
Ser	Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	305	310	315
Leu	His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	325	330	335
Leu	Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	340	345	350
Ala	Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	355	360	365
Glu	Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	370	375	380
Lys	Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	385	390	395
Leu	Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	405	410	415
Thr	Ser	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	420	425	430
Ile	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	435	440	445
Leu	Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Val	Glu	Thr	450	455	460
Val	Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Arg	Asp	Asn	465	470	475
Pro	Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	485	490	495
Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	500	505	510

Asn	Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	515	520	525
Tyr	Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	530	535	540
Pro	Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	545	550	555
Gln	Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	565	570	575
His	Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	580	585	590
Glu	Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	595	600	605
Leu	Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	610	615	620
Ala	Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	625	630	635
Asn	Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	645	650	655
Ala	Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	660	665	670
Pro	Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	675	680	685
Lys	Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	690	695	700
Ser	Thr	Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser	705	710	715
Leu	Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu	725	730	735
Lys	Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn	740	745	750
Ser	Val	Val	Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu	755	760	765
Leu	Met	Cys	Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu	770	775	780
Phe	Thr	Tyr	Trp	Asn	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe	785	790	795
Thr	Ile	Ser	Glu	Val	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg	805	810	815
Tyr	Ile	Ala	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	Leu	Gly	820	825	830

Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
 835 840 845
 Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
 850 855 860
 Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
 865 870 875 880
 Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
 885 890 895
 Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
 900 905 910
 Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
 915 920 925
 Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
 930 935 940
 Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
 945 950 955 960
 Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
 965 970 975
 Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
 980 985 990
 Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
 995 1000 1005
 Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
 1010 1015 1020
 Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
 1025 1030 1035 1040
 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
 1045 1050 1055
 Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
 1060 1065 1070
 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
 1075 1080 1085
 Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
 1090 1095 1100
 His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
 1105 1110 1115 1120
 Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
 1125 1130 1135
 Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
 1140 1145 1150

Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
 1155 1160 1165
 Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
 1170 1175 1180
 Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
 1185 1190 1195 1200
 Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
 1205 1210 1215
 Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
 1220 1225 1230
 Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
 1235 1240 1245
 Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
 1250 1255 1260
 Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
 1265 1270 1275 1280
 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
 1285 1290 1295
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
 1300 1305 1310
 Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
 1315 1320 1325
 Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 1330 1335 1340
 Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
 1345 1350 1355 1360
 Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
 1365 1370 1375
 Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
 1380 1385 1390
 Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
 1395 1400 1405
 Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
 1410 1415 1420
 Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 1425 1430 1435 1440
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 1445 1450 1455
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 1460 1465 1470

Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 1475 1480 1485
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 1490 1495 1500
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 1505 1510 1515 1520
 Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly
 1525 1530

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 <213> Rattus norvegicus

 <220>
 <223> rat TRG

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 Lys Leu Ser Arg Gly His Ser Pro Leu Met Lys Lys Val Phe Asp Val
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 Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
 20 25 30
 Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
 35 40 45
 Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
 50 55 60
 Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln
 65 70 75 80
 Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys
 85 90 95
 Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu
 100 105 110
 Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu
 115 120 125
 Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr
 130 135 140
 Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val
 145 150 155 160
 Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met
 165 170 175
 Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro
 180 185 190
 Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys
 195 200 205

Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	His	Val	Thr	Ala		
210						215					220						
Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Glu	Ala	Asp	Leu	Ala	Leu	Gln		
225					230				235						240		
Arg	Glu	Pro	Pro	Val	Phe	Pro	Tyr	Ser	His	Thr	Ser	Cys	Gln	Arg	Lys		
				245					250					255			
Ser	Arg	Gly	Gly	Met	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile		
			260					265					270				
Thr	Pro	Asn	Ile	Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met		
		275					280					285					
Gln	Asp	Val	His	Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln		
	290					295					300						
Cys	Ala	Asp	Gly	Leu	Trp	Lys	Ala	Glu	Arg	Leu	Arg	Ala	Gly	Leu	Leu		
305					310					315					320		
Thr	Ser	Ile	Asn	Ser	Ser	Ser	Pro	Ser	Met	Lys	Ser	Gly	Gly	Thr	Leu		
			325						330					335			
Glu	Thr	Thr	His	Leu	Tyr	Asp	Thr	Leu	His	Arg	Pro	Tyr	Ser	Lys	Val		
			340					345					350				
Thr	Glu	Val	Ile	Thr	Arg	Ala	Ala	Gly	Ser	Trp	Asp	Leu	Leu	Pro	Gly		
		355					360					365					
Gly	Leu	Phe	Gly	Gln	Gly	Phe	Phe	Glu	Asp	Glu	Asp	Gly	Lys	Glu	Tyr		
	370					375					380						
Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg		
385					390					395					400		
Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met		
				405					410					415			
Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Phe		
			420					425					430				
Ala	Tyr	Ile	Gln	Val	Thr	His	Val	Thr	Pro	Phe	Phe	Asp	Glu	Lys	Glu		
		435					440					445					
Leu	Gln	Glu	Arg	Lys	Thr	Glu	Phe	Glu	Arg	Cys	His	Asn	Ile	Arg	Arg		
	450					455					460						
Phe	Met	Phe	Glu	Met	Pro	Phe	Thr	Gln	Thr	Gly	Lys	Arg	Gln	Gly	Gly		
465					470					475					480		
Val	Glu	Glu	Gln	Cys	Lys	Arg	Arg	Thr	Ile	Leu	Thr	Ala	Ile	His	Cys		
				485					490					495			
Phe	Pro	Tyr	Val	Lys	Lys	Arg	Ile	Pro	Val	Met	Tyr	Gln	His	His	Thr		
			500					505					510				
Asp	Leu	Asn	Pro	Ile	Glu	Val	Ala	Ile	Asp	Glu	Met	Ser	Lys	Lys	Val		
		515					520					525					

Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
 530 535 540
 Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
 545 550 555 560
 Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
 565 570 575
 Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
 580 585 590
 Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
 595 600 605
 Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
 610 615 620
 Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly
 625 630 635 640
 Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln
 645 650 655
 Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu
 660 665 670
 Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val
 675 680 685
 Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln
 690 695 700
 Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr
 705 710 715 720
 Val Ile Phe Asn Ser Arg Phe Tyr Arg Ser Trp Gly Lys Val His Ile
 725 730 735

Phe Phe

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 <212> PRT
 <213> Homo sapiens

<220>
 <223> human CLASP-4

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 Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile
 20 25 30
 Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu
 35 40 45

Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro
 50 55 60
 Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala
 65 70 75 80
 Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile
 85 90 95
 Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Glu Ile Ile Ala Lys
 100 105 110
 Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His
 115 120 125
 Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe
 130 135 140
 Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu
 145 150 155 160
 Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu
 165 170 175
 Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile
 180 185 190
 Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe
 195 200 205
 Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn
 210 215 220
 Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser
 225 230 235 240
 Asn Leu Glu Tyr Ser Leu Ser Asp Glu Tyr Cys Lys His His Phe Leu
 245 250 255
 Val Gly Leu Leu Leu Arg Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr
 260 265 270
 Glu Ile Arg Tyr Thr Ala Ile Ser Val Ile Lys Asn Leu Leu Ile Lys
 275 280 285
 His Ala Phe Asp Thr Arg Tyr Gln His Lys Asn Gln Gln Ala Lys Ile
 290 295 300
 Ala Gln Leu Tyr Leu Pro Phe Val Gly Leu Leu Leu Glu Asn Ile Gln
 305 310 315 320
 Arg Leu Ala Gly Arg Asp Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn
 325 330 335
 Ser Ala Ser Arg Asp Glu Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn
 340 345 350
 Arg Gly Ser Leu Ser Thr Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln
 355 360 365

Asn Gly His Gly Ile Lys Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro
 370 375 380
 Glu Gly Ala Thr Gly Phe Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr
 385 390 395 400
 Arg Gln Ser Ser Thr Arg Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp
 405 410 415
 Gln Tyr Glu Ile Arg Ser Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys
 420 425 430
 Met Ile Ser Glu Asp Thr Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro
 435 440 445
 Gln Glu Leu Ile Asn Ile Leu Ile Leu Leu Glu Val Cys Leu Phe His
 450 455 460
 Phe Arg Tyr Met Gly Lys Arg Asn Ile Ala Arg Val His Asp Ala Trp
 465 470 475 480
 Leu Ser Lys His Phe Gly Ile Asp Arg Lys Ser Gln Thr Met Pro Ala
 485 490 495
 Leu Arg Asn Arg Ser Gly Val Met Gln Ala Arg Leu Gln His Leu Ser
 500 505 510
 Ser Leu Glu Ser Ser Phe Thr Leu Asn His Ser Ser Thr Thr Thr Glu
 515 520 525
 Ala Asp Ile Phe His Gln Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu
 530 535 540
 Val Ser Leu Thr Val Leu Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe
 545 550 555 560
 Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys
 565 570 575
 Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val
 580 585 590
 Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe
 595 600 605
 Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys
 610 615 620
 Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn
 625 630 635 640
 Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr
 645 650 655
 Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala
 660 665 670
 Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe
 675 680 685

Gln	Glu	Ser	Leu	Phe	Ile	Ile	Asn	Asn	Phe	Ala	Asn	Ser	Asp	Arg	Pro	690	695	700
Met	Leu	Ala	Arg	Ala	Phe	Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	705	710	715
Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	725	730	735
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys	Ser	Tyr	740	745	750
Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met	Ala	Lys	755	760	765
Ile	His	Val	Lys	Asn	Gly	Asp	Phe	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Val	770	775	780
His	Val	Ala	Ala	Leu	Val	Ala	Glu	Phe	Leu	His	Arg	Lys	Lys	Leu	Phe	785	790	795
Pro	Asn	Gly	Cys	Ser	Ala	Phe	Lys	Lys	Ile	Thr	Pro	Asn	Ile	Asp	Glu	805	810	815
Glu	Gly	Ala	Met	Lys	Glu	Asp	Ala	Gly	Met	Met	Asp	Val	His	Tyr	Ser	820	825	830
Glu	Glu	Val	Leu	Leu	Glu	Leu	Leu	Glu	Gln	Cys	Val	Asn	Gly	Leu	Trp	835	840	845
Lys	Ala	Glu	Arg	Tyr	Glu	Ile	Ile	Ser	Glu	Ile	Ser	Lys	Leu	Ile	Gly	850	855	860
Pro	Ile	Tyr	Glu	Asn	Arg	Arg	Glu	Phe	Glu	Asn	Leu	Thr	Gln	Val	Tyr	865	870	875
Arg	Thr	Leu	His	Gly	Ala	Tyr	Thr	Lys	Ile	Leu	Glu	Val	Met	His	Thr	885	890	895
Lys	Lys	Arg	Leu	Leu	Gly	Thr	Phe	Phe	Arg	Val	Ala	Phe	Tyr	Gly	Gln	900	905	910
Ser	Phe	Phe	Glu	Glu	Glu	Asp	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	915	920	925
Lys	Leu	Thr	Gly	Leu	Ser	Glu	Ile	Ser	Leu	Arg	Leu	Val	Lys	Leu	Tyr	930	935	940
Gly	Glu	Lys	Phe	Gly	Thr	Glu	Asn	Val	Lys	Ile	Ile	Gln	Asp	Ser	Asp	945	950	955
Lys	Val	Asn	Ala	Lys	Glu	Leu	Asp	Pro	Lys	Tyr	Ala	His	Ile	Gln	Val	965	970	975
Thr	Tyr	Val	Lys	Pro	Tyr	Phe	Asp	Asp	Lys	Glu	Leu	Thr	Glu	Arg	Lys	980	985	990
Thr	Glu	Phe	Glu	Arg	Asn	His	Asn	Ile	Ser	Arg	Phe	Val	Phe	Glu	Ala	995	1000	1005

Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys
 1010 1015 1020
 Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys
 1025 1030 1035 1040
 Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
 1045 1050 1055
 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
 1060 1065 1070
 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
 1075 1080 1085
 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
 1090 1095 1100
 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
 1105 1110 1115 1120
 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
 1125 1130 1135
 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
 1140 1145 1150
 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
 1155 1160 1165
 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
 1170 1175 1180
 Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
 1185 1190 1195 1200
 Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val
 1205 1210

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<213> Homo sapiens

<220>

<223> human CLASP-1

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 Gln Asn Glu Glu Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro
 20 25 30
 Asp Ile Val Ala Lys Cys His Glu Gln Leu Asp His Ser Val Gln
 35 40 45
 Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro
 50 55 60

Val	His	Glu	Asp	Leu	Ala	Lys	Asn	Val	Thr	Gly	Leu	Leu	Lys	Ser	Asn	
65					70					75					80	
Asp	Ser	Pro	Thr	Val	Lys	His	Val	Leu	Lys	His	Ser	Trp	Phe	Phe	Phe	
				85					90					95		
Ala	Ile	Ile	Leu	Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Asp	Thr	Asn	Lys	
			100					105					110			
Ile	Gln	Leu	Pro	Arg	Pro	Gln	Arg	Phe	Pro	Glu	Ser	Tyr	Gln	Asn	Glu	
		115					120					125				
Leu	Asp	Asn	Leu	Val	Met	Val	Leu	Ser	Asp	His	Val	Ile	Trp	Lys	Tyr	
	130					135					140					
Lys	Asp	Ala	Leu	Glu	Glu	Thr	Arg	Arg	Ala	Thr	His	Ser	Val	Ala	Arg	
145					150					155					160	
Phe	Leu	Lys	Arg	Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Cys	Val	Phe	Lys	
				165					170					175		
Met	Val	Asn	Asn	Tyr	Ile	Ser	Met	Phe	Ser	Ser	Gly	Asp	Leu	Lys	Thr	
			180					185					190			
Leu	Cys	Gln	Tyr	Lys	Phe	Asp	Phe	Leu	Gln	Glu	Val	Cys	Gln	His	Glu	
		195					200					205				
His	Phe	Ile	Pro	Leu	Cys	Leu	Pro	Ile	Arg	Ser	Ala	Asn	Ile	Pro	Asp	
	210					215					220					
Pro	Leu	Thr	Pro	Ser	Glu	Ser	Thr	Gln	Glu	Leu	His	Ala	Ser	Asp	Met	
225					230					235					240	
Pro	Glu	Tyr	Ser	Val	Thr	Asn	Glu	Phe	Cys	Arg	Lys	His	Phe	Leu	Ile	
				245					250					255		
Gly	Ile	Leu	Leu	Arg	Glu	Val	Gly	Phe	Ala	Leu	Gln	Glu	Asp	Gln	Asp	
		260					265						270			
Val	Arg	His	Leu	Ala	Leu	Ala	Val	Leu	Lys	Asn	Leu	Met	Ala	Lys	His	
		275					280					285				
Ser	Phe	Asp	Asp	Arg	Tyr	Arg	Glu	Pro	Arg	Lys	Gln	Ala	Gln	Ile	Ala	
	290					295					300					
Ser	Leu	Tyr	Met	Pro	Leu	Tyr	Gly	Met	Leu	Leu	Asp	Asn	Met	Pro	Arg	
305					310					315					320	
Ile	Tyr	Leu	Lys	Asp	Leu	Tyr	Pro	Phe	Thr	Val	Asn	Thr	Ser	Asn	Gln	
				325					330					335		
Gly	Ser	Arg	Asp	Asp	Leu	Ser	Thr	Asn	Gly	Gly	Phe	Gln	Ser	Gln	Thr	
			340					345					350			
Ala	Ile	Lys	His	Ala	Asn	Ser	Val	Asp	Thr	Ser	Phe	Ser	Lys	Asp	Val	
		355					360					365				
Leu	Asn	Ser	Ile	Ala	Ala	Phe	Ser	Ser	Ile	Ala	Ile	Ser	Thr	Val	Asn	
	370					375					380					

His Ala Asp Ser Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser
 385 390 395 400
 Thr Asn Glu Lys Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro
 405 410 415
 Arg Pro Leu Ala Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp
 420 425 430
 Gln Ala Glu Thr Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys
 435 440 445
 Thr Ile Ser Tyr Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser
 450 455 460
 Pro Glu Val Ser Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn
 465 470 475 480
 Phe Arg Tyr Leu Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala
 485 490 495
 Phe Lys Phe Val Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser
 500 505 510
 Asn Pro Ser Cys Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser
 515 520 525
 Thr Ser Arg His Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro
 530 535 540
 Ile Ile Arg Gly Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met
 545 550 555 560
 Leu Asp Asn Thr Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His
 565 570 575
 His Val Asp Thr Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile
 580 585 590
 Leu Asp Leu Val Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln
 595 600 605
 Gln Cys Asp Cys Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr
 610 615 620
 Met Leu Phe Phe Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val
 625 630 635 640
 Phe Ala Ser Leu Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe
 645 650 655
 Gln Gly Pro Ala Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys
 660 665 670
 Cys Cys Asn His Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu
 675 680 685
 Leu Tyr Leu Phe Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser
 690 695 700

Ile	Val	Arg	Ser	His	Leu	Gln	Leu	Ile	Lys	Ala	Val	Ser	Gln	Leu	Ile	705	710	715	720
Ala	Asp	Ala	Gly	Ile	Gly	Gly	Ser	Arg	Phe	Gln	His	Ser	Leu	Ala	Ile	725	730	735	
Thr	Asn	Asn	Phe	Ala	Asn	Gly	Asp	Lys	Gln	Met	Lys	Asn	Ser	Asn	Phe	740	745	750	
Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	755	760	765	
Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	Asp	Pro	Glu	Met	Leu	Val	770	775	780	
Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Asn	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	785	790	795	800
Arg	Arg	Thr	Trp	Leu	Glu	Ser	Met	Ala	Lys	Ile	His	Ala	Arg	Asn	Gly	805	810	815	
Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Ile	His	Ile	Ala	Ala	Leu	Ile	820	825	830	
Ala	Glu	Tyr	Leu	Lys	Arg	Lys	Gly	Tyr	Trp	Lys	Val	Glu	Lys	Ile	Cys	835	840	845	
Thr	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Thr	His	Pro	Cys	Asp	Ser	Asn	Ser	850	855	860	
Leu	Leu	Thr	Thr	Pro	Ser	Gly	Gly	Ser	Met	Phe	Ser	Met	Gly	Trp	Pro	865	870	875	880
Ala	Phe	Leu	Ser	Ile	Thr	Pro	Asn	Ile	Lys	Glu	Glu	Gly	Ala	Ala	Lys	885	890	895	
Glu	Asp	Ser	Gly	Met	His	Asp	Thr	Pro	Tyr	Asn	Glu	Asn	Ile	Leu	Val	900	905	910	
Glu	Gln	Leu	Tyr	Met	Cys	Gly	Glu	Phe	Leu	Trp	Lys	Ser	Glu	Arg	Tyr	915	920	925	
Glu	Leu	Ile	Ala	Asp	Val	Asn	Lys	Pro	Ile	Ile	Ala	Val	Phe	Glu	Lys	930	935	940	
Gln	Arg	Asp	Phe	Lys	Lys	Leu	Ser	Asp	Leu	Tyr	Tyr	Asp	Ile	His	Arg	945	950	955	960
Ser	Tyr	Leu	Lys	Val	Ala	Glu	Val	Val	Asn	Ser	Glu	Lys	Arg	Leu	Phe	965	970	975	
Gly	Arg	Tyr	Tyr	Arg	Val	Ala	Phe	Tyr	Gly	Gln	Gly	Phe	Phe	Glu	Glu	980	985	990	
Glu	Glu	Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Gly	Leu	995	1000	1005	
Ser	Glu	Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu	Tyr	Ala	Asp	Lys	Phe	Gly	1010	1015	1020	

Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
 1025 1030 1035 1040
 Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
 1045 1050 1055
 Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
 1060 1065 1070
 His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
 1075 1080 1085
 Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
 1090 1095 1100
 Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
 1105 1110 1115 1120
 Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
 1125 1130 1135
 Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
 1140 1145 1150
 Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
 1155 1160 1165
 Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
 1170 1175 1180
 Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
 1185 1190 1195 1200
 Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
 1205 1210 1215
 Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
 1220 1225 1230
 Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn
 1235 1240 1245
 Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
 1250 1255 1260
 Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val
 1265 1270 1275 1280
 Ser Ile Ser Ser Ser Ala Glu Val
 1285

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<220>
 <223> human CLASP-3

<400> 14

Gly Pro Gly Pro Ala Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn
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Ser Ala Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp
20 25 30
Ile Ser Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile
35 40 45
Gly Ser Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly
50 55 60
Pro Lys Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser
65 70 75 80
Thr Gln Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu
85 90 95
Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys
100 105 110
Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser
115 120 125
Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met
130 135 140
Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala
145 150 155 160
Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala
165 170 175
Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp
180 185 190
Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn
195 200 205
Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys
210 215 220
Ser Cys Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro
225 230 235 240
Ser Val Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser
245 250 255
His Glu His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro
260 265 270
Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser
275 280 285
Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu
290 295 300
Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu
305 310 315 320

Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly
 325 330 335
 Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His
 340 345 350
 Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala
 355 360 365
 Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln
 370 375 380
 Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys
 385 390 395 400
 Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln
 405 410 415
 Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg
 420 425 430
 Pro Gly Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr
 435 440 445
 Phe Ser Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val
 450 455 460
 Leu Lys Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu
 465 470 475 480
 Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val
 485 490 495
 Ser Cys Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser
 500 505 510
 Leu Thr Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala
 515 520 525
 Ile Leu Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg
 530 535 540
 Gly Gln Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu
 545 550 555 560
 Asn Leu Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu
 565 570 575
 Lys Leu Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp
 580 585 590
 Gly Asn Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu
 595 600 605
 Ile Val Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu
 610 615 620
 Gly Gly Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser
 625 630 635 640

Ala	Val	Tyr	Leu	Gln	His	Cys	Phe	Ala	Thr	Gln	Arg	Ala	Leu	Val	Ser	645	650	655
Lys	Phe	Pro	Glu	Leu	Leu	Phe	Glu	Glu	Glu	Thr	Glu	Gln	Cys	Ala	Asp	660	665	670
Leu	Cys	Leu	Arg	Leu	Leu	Arg	His	Cys	Ser	Ser	Ser	Ile	Gly	Thr	Ile	675	680	685
Arg	Ser	His	Pro	Ser	Ala	Ser	Leu	Tyr	Leu	Leu	Met	Arg	Gln	Asn	Phe	690	695	700
Glu	Ile	Gly	Asn	Asn	Phe	Ala	Arg	Val	Lys	Met	Gln	Val	Pro	Met	Ser	705	710	715
Leu	Ser	Ser	Leu	Val	Gly	Thr	Ser	Gln	Asn	Phe	Asn	Glu	Glu	Phe	Leu	725	730	735
Arg	Arg	Ser	Leu	Lys	Thr	Ile	Leu	Thr	Tyr	Ala	Glu	Glu	Asp	Leu	Glu	740	745	750
Leu	Arg	Glu	Thr	Thr	Phe	Pro	Asp	Gln	Val	Gln	Asp	Leu	Val	Phe	Asn	755	760	765
Leu	His	Met	Ile	Leu	Ser	Asp	Thr	Val	Lys	Met	Lys	Glu	His	Gln	Glu	770	775	780
Asp	Pro	Glu	Met	Leu	Ile	Asp	Leu	Met	Tyr	Arg	Ile	Ala	Lys	Gly	Tyr	785	790	795
Gln	Thr	Ser	Pro	Asp	Leu	Arg	Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	805	810	815
Lys	His	Ser	Glu	Arg	Ser	Asn	His	Ala	Glu	Ala	Ala	Gln	Cys	Leu	Val	820	825	830
His	Ser	Ala	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Ser	Met	Leu	Glu	Asp	Arg	835	840	845
Lys	Tyr	Leu	Pro	Val	Gly	Cys	Val	Thr	Phe	Gln	Asn	Ile	Ser	Ser	Asn	850	855	860
Val	Leu	Glu	Glu	Ser	Ala	Val	Ser	Asp	Asp	Val	Val	Ser	Pro	Asp	Glu	865	870	875
Glu	Gly	Ile	Cys	Ser	Gly	Lys	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly	885	890	895
Leu	Leu	Glu	Gln	Ala	Ala	Ala	Ser	Phe	Ser	Met	Ala	Gly	Met	Tyr	Glu	900	905	910
Ala	Val	Asn	Glu	Val	Tyr	Lys	Val	Leu	Ile	Pro	Ile	His	Glu	Ala	Asn	915	920	925
Arg	Asp	Ala	Lys	Lys	Leu	Ser	Thr	Ile	His	Gly	Lys	Leu	Gln	Glu	Ala	930	935	940
Phe	Ser	Lys	Ile	Val	His	Gln	Ser	Thr	Gly	Trp	Glu	Arg	Met	Phe	Gly	945	950	955
																		960

Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp
 965 970 975
 Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu
 980 985 990
 Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp
 995 1000 1005
 Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu
 1010 1015 1020
 Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe
 1025 1030 1035 1040
 Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr
 1045 1050 1055
 Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg
 1060 1065 1070
 Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr
 1075 1080 1085
 Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His
 1090 1095 1100
 Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met
 1105 1110 1115 1120
 Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala
 1125 1130 1135
 Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr
 1140 1145 1150
 Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile
 1155 1160 1165
 Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys
 1170 1175 1180
 Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys
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 Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys
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 Leu Ser Ser Pro
 1220

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 <220>
 <223> human CLASP-5

<400> 15
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Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser
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Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro
35 40 45
Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu
50 55 60
Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu
65 70 75 80
Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys
85 90 95
Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp
100 105 110
Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr
115 120 125
Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr
130 135 140
Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr
145 150 155 160
Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu
165 170 175
Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met
180 185 190
Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro
195 200 205
Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu
210 215 220
Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln
225 230 235 240
Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu Glu Glu Ala Leu
245 250 255
Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg Arg Arg Ala Pro
260 265 270
Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu Arg Trp Lys Lys
275 280 285
Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu Asp Lys Thr Lys
290 295 300
Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn Leu Ala Thr Glu
305 310 315 320

Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile Ile Gln Ala Ser
 325 330 335
 Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly Val Leu Arg Val
 340 345 350
 Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr Tyr Leu Thr His
 355 360 365
 Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp Leu Leu
 370 375 380
 Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln Val Leu
 385 390 395 400
 His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser Gln Ala Cys Ala
 405 410 415
 Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser Asn Phe
 420 425 430
 Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu Val Gly
 435 440 445
 Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu Arg Thr
 450 455 460
 Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr Pro Phe
 465 470 475 480
 Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile Leu Tyr
 485 490 495
 Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met Leu Met
 500 505 510
 Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro Asp Leu
 515 520 525
 Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys Lys Lys
 530 535 540
 Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala Leu Val
 545 550 555 560
 Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro Val Gly
 565 570 575
 Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Val
 580 585 590
 Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys Ala Gly
 595 600 605
 Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala
 610 615 620
 Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu Val Tyr
 625 630 635 640

Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg Lys Leu
 645 650 655
 Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile Val Asn
 660 665 670
 Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Phe
 675 680 685
 Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu
 690 695 700
 Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu Ala Phe
 705 710 715 720
 Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val Ile Lys Asp Ser
 725 730 735
 Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
 740 745 750
 Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys Asp Arg
 755 760 765
 Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met Tyr Thr
 770 775 780
 Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His Glu Gln
 785 790 795 800
 Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile
 805 810 815
 Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro
 820 825 830
 Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
 835 840 845
 Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln Met Val
 850 855 860
 Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu Glu Val
 865 870 875 880
 Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu Tyr Arg
 885 890 895
 His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met Arg Cys
 900 905 910
 Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg
 915 920 925
 Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn
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 Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile
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Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe
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Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
 980 985

<210> 16
 <211> 24
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-1

<400> 16
 Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly
 1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
 20

<210> 17
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human KIAA1058

<400> 17
 Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp
 1 5 10 15

Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu
 20 25 30

Tyr Ile Tyr Lys Glu Pro
 35

<210> 18
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motifs A
 and B from human CLASP-2

<400> 18
 Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 1 5 10

<210> 19
<211> 24
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-6

<400> 19

Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
20

<210> 20
<211> 24
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-4

<400> 20

Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
1 5 10 15

Lys Glu Tyr Ile Tyr Lys Glu Pro
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<210> 21
<211> 31
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK180

<400> 21

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 22
<211> 31
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK2

<400> 22

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
1 5 10 15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
20 25 30

<210> 23

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from canonical DOCK3

<400> 23

Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Tyr Val Cys Arg Gly His
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<210> 24

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human KIAA0716

<400> 24

Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
1 5 10 15

Lys Glu Phe Val Cys Arg Gly His
20

<210> 25

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A
and B from human CLASP-3

<400> 25

Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
1 5 10 15

Glu Phe Val Tyr Lys Glu Pro
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<210> 26
<211> 60
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C
from rat TRG

<400> 26

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
35 40 45

Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
50 55 60

<210> 27
<211> 60
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<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-1

<400> 27

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
20 25 30

Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
35 40 45

Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
50 55 60

<210> 28
<211> 60
<212> PRT
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<220>

<223> Description of Artificial Sequence:DOCK motif C
from human CLASP-2

<400> 28

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
1 5 10 15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
 35 40 45

Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
 50 55 60

<210> 29
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human CLASP-4

<400> 29
 Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
 1 5 10 15

Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
 20 25 30

Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
 35 40 45

Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
 50 55 60

<210> 30
 <211> 60
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human CLASP-3

<400> 30
 Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
 1 5 10 15

Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
 20 25 30

Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
 35 40 45

Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu
 50 55 60

<210> 31
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<220>
 <223> Description of Artificial Sequence:DOCK motif C
 from human KIAA0716

<400> 31

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
1 5 10 15

Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
20 25 30

Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45

Ile Pro Glu Ser Gln Glu
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<210> 32

<211> 54

<212> PRT

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<220>

<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK3

<400> 32

His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
1 5 10 15

Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
20 25 30

Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
35 40 45

Ile Pro Asp Tyr Val Asp
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<210> 33

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<212> PRT

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<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK2

<400> 33

Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
20 25 30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro
35 40 45

<210> 34

<211> 53

<212> PRT

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<223> Description of Artificial Sequence:DOCK motif C
from canonical DOCK180

<400> 34

Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
1 5 10 15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
20 25 30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
35 40 45

Leu Asp Glu His Pro
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<210> 35

<211> 45

<212> PRT

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<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-1

<400> 35

Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
35 40 45

<210> 36

<211> 45

<212> PRT

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<223> Description of Artificial Sequence:DOCK motifs D
and E from rat TRG

<400> 36

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His
35 40 45

<210> 37
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<223> Description of Artificial Sequence:DOCK motifs D
and E from human KIAA1058

<400> 37
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40 45

<210> 38
<211> 45
<212> PRT
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<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-2

<400> 38
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40 45

<210> 39
<211> 44
<212> PRT
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<220>
<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-6

<400> 39
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
20 25 30
His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
35 40

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<212> PRT
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<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-4

<400> 40

Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
1 5 10 15
Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
20 25 30
Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
35 40 45

<210> 41
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<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-3

<400> 41

Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
1 5 10 15
Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
20 25 30
Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
35 40 45

<210> 42
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<223> Description of Artificial Sequence:DOCK motifs D
and E from human CLASP-5

<400> 42

Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
1 5 10 15
Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val
20 25 30
Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
35 40 45

<210> 43
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<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from human KIAA0716

<400> 43
 Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
 1 5 10 15
 Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
 35 40 45

<210> 44
 <211> 45
 <212> PRT
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 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK2

<400> 44
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15
 Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

<210> 45
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 <212> PRT
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<220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK3

<400> 45
 Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
 1 5 10 15
 Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg
 35 40 45

<210> 46
 <211> 45
 <212> PRT
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 <220>
 <223> Description of Artificial Sequence:DOCK motifs D
 and E from canonical DOCK180

 <400> 46
 Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1 5 10 15
 Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
 20 25 30
 Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
 35 40 45

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 <211> 58
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 <223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-1

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 Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
 1 5 10 15
 Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
 20 25 30
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 35 40 45
 Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
 50 55

 <210> 48
 <211> 58
 <212> PRT
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 <220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from rat TRG

 <400> 48
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
 20 25 30
 Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
 35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 49
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<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human KIAA1058

<400> 49
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15
Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
20 25 30
Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45
Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 50
<211> 58
<212> PRT
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<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-2

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Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
1 5 10 15
Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
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Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
35 40 45
Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
50 55

<210> 51
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:DOCK motifs F
and G from human CLASP-6

<400> 51
 Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
 20 25 30
 Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
 35 40 45
 Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
 50 55

<210> 52
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 and G from human CLASP-3

<400> 52
 Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
 1 5 10 15
 Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
 20 25 30
 Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
 35 40 45
 Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
 50 55

<210> 53
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 <212> PRT
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<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-4

<400> 53
 Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
 1 5 10 15
 Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
 20 25 30
 Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys
 35 40 45
 Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu
 50 55

<210> 54
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 <212> PRT
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<223> Description of Artificial Sequence:DOCK motifs F
 and G from human CLASP-5

<400> 54

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln
 1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp
 20 25 30

Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
 35 40 45

Phe Ile Met Arg Cys Gly Glu Ala Val Glu
 50 55

<210> 55
 <211> 60
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<220>

<223> Description of Artificial Sequence:DOCK motifs F
 and G from human KIAA0716

<400> 55

Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1 5 10 15

Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu
 20 25 30

Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
 35 40 45

Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
 50 55 60

<210> 56
 <211> 60
 <212> PRT
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<223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK2

<400> 56

Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1 5 10 15

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30

Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
 35 40 45

Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
 50 55 60

<210> 57
 <211> 60
 <212> PRT
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<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK3

<400> 57
 Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1 5 10 15

Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn
 20 25 30

Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met
 35 40 45

Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
 50 55 60

<210> 58
 <211> 60
 <212> PRT
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<220>
 <223> Description of Artificial Sequence:DOCK motifs F
 and G from canonical DOCK180

<400> 58
 Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1 5 10 15

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
 20 25 30

Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile
 35 40 45

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 50 55 60

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Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys
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aag ctt ttt cac gag gag ctg gct ttg cag tgg gtt gtt tgc agt ggc 328
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Ser Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu
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Met Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu
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Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala
              80              85              90

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Ala Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys
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Asn Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile
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Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn
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Pro Ser Val Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys
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205 210 215 220	
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Glu Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val	
225 230 235	
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Gly Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser	
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His Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val	
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Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro	
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Gln Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile	
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Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser	
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Gln Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr	
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Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu Ile Cys Leu Leu Trp	
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Leu Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys	
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Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile	
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Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu	
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Glu Ile Val Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile	
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Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp	
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Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp	
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Gly Leu Leu Glu Gln Ala Ala Ser Phe Ser Met Ala Gly Met Tyr	
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830 835 840	
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Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu	
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Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe	
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Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu	
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Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala	
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Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn	
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Arg Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu	
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Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro	
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Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr	
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Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu	
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Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn	
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Lys Leu Ser Ser Pro	
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 85 90 95
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 Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser His Glu His
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 Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser
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 sequence of bacterial artificial chromosome BAC8
 using primer C3S3

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<222> (1)..(755)

<223> n = g, a, c or t

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gcgctnccnn ntnntttatc ttctgaaaag actnatatna ttctatgatt ataacattac 60
acactctaac actggacttn ttaaataatgg atgtaattaa tagatgactg aatatttttag 120
cttctcaaatt atnttttaang tcctacaat gtttgnatnt gcttaaaata aaatanaaaa 180
ccccatatta ctttcagaaa antatgctag ctaacaatag gacanaaaaa ttctgtgtat 240
gcaacaaaaa aaaattcaac cttnaatctt cttttttttc caatanaaaa cagggctact 300
ctgccacagg ctggagtcag tggctgatac agctactgca gctcactccg ggctatgtga 360
ttgcctgcct aagcctcnga gtagtaggct caggtgccac tacatgccag taatctaaaa 420
tttatagaga cagggctgct gtgtgnccag gctggctaac tccgggctaa gcgttcttgc 480
ctngctctaa atgtgggata cagnatgtat catncatcag ccaaaaagtt aattaanttc 540
cagatnanta tttgcatcaa agctccaatn tagcttgaag tagaacctgc tcnttggcta 600
gantatcccc nntgttatgg atcatattan gcnnctgtga tgccgaatgg natctattcc 660
gggagacana ttactatngg atganagcan atngcccnna tgcttntttg taacgctnna 720
nntaagaacn ttctngacat cgtcatagnt cgaagtnntn ngcganttga tactaanttc 780
atgntangcc natgactntn gtgattnttg antgntcggg agaacctacn tncnccntac 840
nnatannctn caccnccctac tactntnncn ntcnctctct anttctactc cacnttatta 900
tcctcnncct tcncatcntc ccactntnat tcnacgcnc nanacttanc nttnatncac 960
```


<210> 65
 <211> 722
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 3.1
 sequence of bacterial artificial chromosome BAC8
 using primer C3AS4

<220>
 <221> modified_base
 <222> (1)..(722)
 <223> n = g, a, c or t

<400> 65
 taatgtacat agtgctcatg actgcagatg attcgtagaa aatccagcct caaggacacc 60
 agaacactgg gattcggtaa tgagtaaagc tttgaagaca ccttgtaagc aatgcataag 120
 taagagaaca ccaattgaat ctattatttc ttttaacta ataccagaat ggcaaattag 180
 aattaaagag atagtacttg gtatccagtt tgggttttgt ggcttaagta gcagtatcac 240
 ctttttccag agttactgct aaaattaaaa attttaaact atcaggttta ctgtataaac 300
 atatttgact aacctaanaag ccacattctt gtatttccaa tatagcatca atatttctac 360
 ttctcataaa acagggaaaa cgtatatcac caaaaataac ttcttattac ttccttctta 420
 aaagaaatta tcaattcttt ttatagcact ttgtgcttac ctgtatttat aatttgtctg 480
 ttttctcagc aacatcataa gctacttgag gagacatact ataaactgat ttaacagctt 540
 tagtgtccct acagcttagc tcaatgtttg acaaatatag gagatcaatg cttaaaggaa 600
 taaaggccag gacaagttct ggtagcaaat agtccataaa aggttttggg ggaaaaggg 660
 aaaaatggat acatatcggg gtngcaagnt ttttccatgt ggggtgaggt gccccatgcc 720
 tt 722

<210> 66
 <211> 783
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 3.2
 sequence of bacterial artificial chromosome BAC9
 using primer C3AS4

<220>
 <221> modified_base
 <222> (1)..(783)
 <223> n = g, a, c or t

<400> 66
 taacatagtg ctctgactgc agatgattcg tagaaaatcc agcctcaagg acaccagaac 60
 actgggattc ggtaatgagt aaagctttga agacaccttg taagcaatgc ataagtaaga 120
 gaacaccaat tgaatctatt atttctttta tactaatacc agaatggcaa attagaatta 180
 aagagatagt acttggatc cagtttgggt tttgtggctt aagtagcagt atcacctttt 240
 tccagagtta ctgctaaaaa taaaaatttt aaactatcag gtttactgta taaacatatt 300
 tgactaacct aaaagccaca ttcttgtatt tccaatatag catcaatatt tctacttctc 360
 ataaaacagg gaaaacgtat ntcacaaaaa ataacttctt attacttcct tcttaaaaag 420
 aaattatcaa ttctttttat agcactttgt gcttaccctg natttataat ttgnctgntt 480
 ttctcagcaa acatcataag ctacttgagg gagacatact attaaacctg attacagctt 540
 ttangtgcc ctacagctta actcaatgtt ttgcaaaatn tnnngagatc aatggcttta 600
 aagaataaaa gancagggac aagttntggg tngccatnag nacaataaag gttttngggg 660

```

gaaaagggaa aaaatngatt ncatntcgng gttngcaagg tnttttccat tgnngggngg 720
aggggccccat gccataantt ttaacctttc ttttttngaa gaaattaaac nnttaaaggg 780
gtn 783

```

```

<210> 67
<211> 721
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 4.1
sequence of bacterial artificial chromosome BAC8
using primer HC3AS6

```

```

<220>
<221> modified_base
<222> (1)..(721)
<223> n = g, a, c or t

```

```

<400> 67
ccagtctgca atatgctgtg cgaagccgat atcaactttg catctttgtc ttgncattcg 60
agaaatcaga cttgtggaag taggagacag cttacagcgt gcacaagctc tcagcagagc 120
atatacgaat gaatcttttc cagggagtta tttatatact acctgagcaa gccactttag 180
ctttgggcag gaacttntgg atgttataag taatacttat atgaataata tgaaattaat 240
atttacttct tttacantct tctcttttcc ttatcttagc ctttatcccc ttgtggaaaa 300
gacactatca atgctagatn ctcccaagnc agagaattat gcaggtttgg tcagagaatc 360
gacacagaca tgtttacaga ttcttcttga aatacatatt gtgcacgagt tttttacant 420
atctcaattt agatctcaga cagcatntng actagnnggt ctaggacata gatacatntt 480
tgngaacttc tatagaanaa cntntgcntt aaaaaggagc ttgttngana ngaatnnnct 540
gnngaaggcc cgatacgana atttgacttc ggngaaaatt nnnnggattnn tacaaaanttc 600
tagngggcac cttnaaaang nntgggnacn ttggnggcgg aaaaaaagcc cttcntttag 660
ntntcccnga aatggaaaag tnccaanttc cnaaaaaaan gggctttgtt nncttncnan 720
a 721

```

```

<210> 68
<211> 921
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 4.2
sequence of bacterial artificial chromosome BAC9
using primer HC3AS6

```

```

<220>
<221> modified_base
<222> (1)..(921)
<223> n = g, a, c or t

```

```

<400> 68
gacgccagct ctgtacacag tctgcaatat gctgtgcgga aggccgatat caactattgc 60
atctttgtct ngncatcgag aaatcagact ctgtggaagn aggcagacaa gactatacag 120
cntgcacana gcatctcagc aggcataata gaatgaanct tttccaggga gttatttata 180
tactacctga gcaagnactt caacttnggc aggaacttgt ggatgnttat aagtatactt 240
atatgaataa natngaaatt aatatttaatt tcttttactt cttctctttt ctttatctta 300
gccttttatcc cctcgtgaaa aagagcacta atcaatgcta ttncnccaa gncaggaatt 360
tatagcaggt tggctcgagaa tcgacacgac atgtttacag antcatcttg aatacatnat 420
tgtgcacgag tnttttactc tatctcaaaa tatagatctc agatcgtcta tngantatgn 480
ggttctagga catgattaca tttttnggga acttccatag aataaacntn tacctnaaaa 540

```

```

nangagcctg ttngaaatng aatctactnc taaagggcna gtnccanatt ttacttccgc 600
ganatntcng gatgttacaa gtctaggggg nctttagnac gttngatntt tgancggaaa 660
aaagcccttc tannggtcnc ctaatggaag cgccaattcc naanaaggnc tgtgtnttn 720
gacatttacc ngnnccnttt ctaatcaaac ntntctttct nnnanccnca ncnncnncc 780
atannccat cncctcnnctn nntctntcac tctcnnnct ntcttcntt ctncactntn 840
nmntcncntn natnnncttc tccnatcct ctcannnnnt canntccct acnntncncn 900
tnttaccatc tncnccnncc t 921

```

<210> 69

<211> 628

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ref 5.1
sequence of bacterial artificial chromosome BAC8
using primer C3S6

<220>

<221> modified_base

<222> (1)..(628)

<223> n = g, a, c or t

<400> 69

```

gtatgatccg ccagaccgct gccatggcaa tngtagggac atcggtccct caactaacia 60
ggcctggcag tttcctnctc acgtcaacgg tcaaaacaat ccttctacag aatttttttt 120
tctngaaaga caaatattta ctaggatatg cccttaaata tatgagatga ttgtatcagc 180
tgatgcaaaa gtgctcagtt ttatttatga aaatattaaa gtcccagaa tattaactgt 240
cttctcccaa acagttttta aaaatgatta cctcaagggt tatgggaaaa agccccgtat 300
tctgcattca gaatttgga aattgcctca ttatagatag ccatntcttt tttttntttt 360
ttttatnctt caagtcttag ggnacatgtg cacaacatgc aggntagtta catatgtata 420
catgtgccat gttggtgtgc tgcacccann aaccgcgaat ttaacattag gtntatctcc 480
aaatgctatc cnttcaccct tcccccatnc cacaacaagg ccccgggcnt tgngatgttc 540
cccttcctgt gccactgtg tntcacattn ccncttcccn cccttantnn ngtgcagaac 600
ntngccngtn gccctntntt tttnnccc 628

```

<210> 70

<211> 953

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ref 5.2
sequence of bacterial artificial chromosome BAC9
using primer C3S6

<220>

<221> modified_base

<222> (1)..(953)

<223> n = g, a, c or t

<400> 70

```

ccnctgatga ttatgaaagt gagagcggaa gtatgataag ccagaccggt gccatggcaa 60
tcgcagggac atcggtccct caactaacia ggcctggcag tttcctcctc acgtcaacgg 120
taaaaacaat cctcctacag aatttttttt tctagaaaga caaatattta ctaggatatg 180
cccttaaata tatgagatga ttgtatcagc ttgatgcaaa aagtgtcag gttttatatt 240
gaaaatatta aagttccaga atattttaact gtcttctccc aacagtttta aaaaatgata 300
cctcagggtt atggggaaaa aagccccgta ttctgtcatt cagaaatttg gaaaatttgn 360
ctcattatag atagttcatt ttcttttttt tttttttttt ttatacnntt aaagttttta 420

```

```

agggggnacca tgttgcacca aanattgcag ggggttngggt accattatgg ttattnccat 480
tggtntcccc antgtttggg gngttggctt tgccaccccc cagngtaaaa ccnnccgntg 540
cgaatttttta aaacaanttt tgggggttat tanttntttc caaaaaatng gcntttttnc 600
ccttttcccc cctttcnccc ncccnnttcc caacnnanca agggggcccc cggttantgg 660
gggaatagnt tccccccct tncctngnn gggccaattg tggggnnnct ccatttggnn 720
tgcaaanctt cccacccnt nattgttggg ggngaaacca tttcccgggg ggtttggggg 780
tttttttttg tccccnttgc ccaantaatt tttgcnttga anaaaaagaa tgggggtttc 840
caaagctttt ngtnccatt tgntcccttt anggnncnt tngttcncct tnccanaang 900
ggccaatgtg aaacnncctt tcattttttt ttattggggg tnccnttat ggn 953

```

```

<210> 71
<211> 683
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 6.1
sequence of bacterial artificial chromosome BAC8
using primer C3S7

```

```

<220>
<221> modified_base
<222> (1)..(683)
<223> n = g, a, c or t

```

```

<400> 71
ttcttgggag cataggtgcc aggcaagaaa tggtagcgcg aagccgagga cagctcggtg 60
cgtacacaat agcttctcct cctggtgaga atttcttcaa ttcccttgag ttgtatattg 120
taatgatcat tgttgctagt cttcaatgtc aatcctatgc tttttaaaaa gtgttttaag 180
tgtaactgtg aattaacttg aataatcatt tctctgcagt aataaaaagt agaattctga 240
tttaggtgag tcagcatacc gccccccccc ccgttttctc tagaaagtct tctctagaaa 300
acgttctcta gaaagtccta tctagaaaac tttctctaga aagtccttat gtgattaata 360
gcatccatcc tcccttttta aatagacttt atttttgtag agcagtttta agttcacagc 420
aaaagtgagc aaaggtacag agatttccca tataccctt agtatgcgta gcctccccc 480
ttattaacat ccccatcaa gagtagtgca tttgttgtaa ctggtgaacc tacattaaca 540
catcatcacc cagagtcgag agtttacatt agggatcatt catataacat ctatttttac 600
tttttttttt ttagttgaga caagattctc gctctgtcac ccaagctgga gtgcagtcg 660
ngtggattgt nggcttactg ncn 683

```

```

<210> 72
<211> 807
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 6.2
sequence of bacterial artificial chromosome BAC9
using primer C3S7

```

```

<220>
<221> modified_base
<222> (1)..(807)
<223> n = g, a, c or t

```

```

<400> 72
gtgccggcaa gaaatggtac ggcgaagccg aggacagctc ggtacgtaca caatagcttc 60
tcctcctggt gagaatttct tcaatttcct tgagttgtat attgtaatga tcattgttgc 120
tagtcttcaa tgtcaatcct atgcttttta aaaagtgttt taagtgtaac tgngaattaa 180
cttgaataat catttctctg cagtaataaa agttagaatt ctgatttagg tgagtcagca 240

```

```

taccgcccc cccccgttt tctctagaaa gtcttctcta gaaaacgttc tctagaaagt 300
cctctctaga aaactttctc tagaaagtcc ttatgtgatt aatagcatcc atcctccctt 360
tttaaataag actttatttt tgtagagcag ttttaagttc acagcaaaaag tgagcaaagg 420
gcagagattt cccatatacc ccttagtatg cgtagcctcc cccattatta acatcccat 480
cagagtaagn gcatttggtg taactggnga acctacaatt nacacattnt naccacacag 540
tcccgaggt ttacatttat gggatcattc ccctantaac acctattttt ttactttttt 600
tttttttttag gttgagacaa gaattttcgg cttcttggtg acccccaaac tnggtagtag 660
ncnnaccgtc gngnaatttn tggggtttcn tngngnnncan tttgtgcnnn cnnctttnncn 720
ccnaaagaan ttttttttca cccttttttt tccccnaan anannancct tccccttggn 780
ggangctggg gacttcnca gnggngg 807

```

```

<210> 73
<211> 721
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 7.1
sequence of bacterial artificial chromosome BAC8
using primer C3S8

```

```

<220>
<221> modified_base
<222> (1)..(721)
<223> n = g, a, c or t

```

```

<400> 73
caaagtgcag tttatctcaa cactgttttg ctacacagaga gccttggttt caaaggtagg 60
ttattttgta cctgcagtgt tgtcagactt tgtttttttt attaacattg tctaagatca 120
tttgacacat tcattgggta atatatgtag taatatatta atgaatatgt gtagttaaaa 180
tttaaataat aacctaagac ccttaattct tctttgcctc tctactgctg cctgcctttt 240
agaatttttc atttattcga atcaccttta accagttctg gtttgaaaaa cagtaacttg 300
gatgtggaga agggcctgaa attaatagcc aatcttaaatt atgggggcttc tcttgttttc 360
tcttcacttg gttctgtttt tataaaaaaac tcaatttata aagaattcaa tatataagca 420
attcaaccca ctgaaattat tttatgatga atggaaaaga aggtatgtgt ttgttcaact 480
gctttaaatg tttacttctt atatttgttt tcccttagaa atatgtatat tcttaaattt 540
tgaaggtagc tatttcattt taatcatcct agaggatgga atgcanagat gttggatgaa 600
aataacttac gtattatttt gtaataaata taagaattca tatatgggtg attacctaag 660
tggttttatg cacattctga tagaaagctt caccaacaat cccttgntng atatattatt 720
t 721

```

```

<210> 74
<211> 836
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 7.2
sequence of bacterial artificial chromosome BAC9
using primer C3S8

```

```

<220>
<221> modified_base
<222> (1)..(836)
<223> n = g, a, c or t

```

```

<400> 74
aagtcagttt atctacaaca ctgttttgct acacagagag ccttggtttc aaaggtagg 60
tattttgtac ctgcagtgtt gtcagacttt gtttttttta ttaacattgt ctaagatcat 120

```

```

ttgacacatt cattgggttaa tatatgtagt aatatattaa tgaatatgtg tagttaaaat 180
ttaaataata acctaagacc cttaattctt ctttgccctc ctactgctgc ctgcctttta 240
gaatttttca tttattcgaa tcacctttta ccagttcttg tttgaaaaac agtaacttgg 300
atgtgggagaa gggcctgaaa ttaatagcca atcttaaata tggggccttct cttgntttct 360
cttcacttgg ttctgttttt ataaaaaact caatttataa agaattcaat atataagcca 420
ttcacccact gaaattatct tatgatgaat ggaaaagaaa ggtatgtgtt tgttcacctg 480
ctttaaaatg ngacntcnta atattttggn tttccctcta agaaaatatg tataatcctt 540
aaaantttng aaagggganc tantttcatt ttttnaatca atcctaanaa ggattgggaa 600
atgcncaga ttttttgatt gaaaaanaac cttancgnat ttaatttttn ggnaataaaa 660
taattagnaa ttccntatta tgnttngaag tacctaaagt ggtttttatt gccccatttc 720
nttgatatgn aaagcctttc accaaccaaa tttcccnttg nnaggaatat tattttttna 780
ngggcctcnt ntttgtgggg ntggaagaaa aaacctttgt tccaaagggc cccnc 836

```

```

<210> 75
<211> 678
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 8.1
sequence of bacterial artificial chromosome BAC8
using primer C3S10

```

```

<220>
<221> modified_base
<222> (1)..(678)
<223> n = g, a, c or t

```

```

<400> 75
agtgttagtc ctcagcagca cttgttgctg aatatttgag catgctggag gaccggaaat 60
atcttcctgt gggatgtgta acatttcagg taggaatctt ccagatgtac attaaatcaa 120
ggtatatctt tttttgggtt tagcttttct cactgggtgt tagatttttt tagtttataa 180
ggaaagctta aagacttaag ccaatgcttc acaaggtgaa ttaacatttc acagtgtattg 240
tcattaatac atttttaagg agtacttctt gttgattctc tttccacagt ttcttacctc 300
tgaattatca gcactatgct tatttattct ctttggtctt actgncttgn aatcccgtta 360
catactttta catctatgga aatgtattac tgataatcag aattcagtag aaattcttaa 420
ttggcctttta cttcacatag cagatatacc aacattctct attccctaca taaaatatta 480
agattatttt atgactaata cccatgactc acagatgagt ttgccctcta gtaggggtcat 540
aattctgacc cactagtgtg attctctgct taccaagagn cagggtatgct tgctttttct 600
tcaaaacctg ttaaatagta ggnttgggga tattntaaaa attaggtaaa tggtatatct 660
tctggtggaa ancagaan 678

```

```

<210> 76
<211> 825
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Ref 8.2
sequence of bacterial artificial chromosome BAC9
using primer C3S10

```

```

<220>
<221> modified_base
<222> (1)..(825)
<223> n = g, a, c or t

```

```

<400> 76
cagcagcact tggttgctgaa tatttgagca tgctggagga ccggaaatat cttcctgtgg 60

```

```

gatgtgtaac atttcaggta ggaatcttcc agatgtacat taaatcaagg tatatctttt 120
tttggtttta gcttttctca ctgggtgttta gattttttta gtttataagg aaagcttaaa 180
gacttaagcc aatgcttcac aagggtgaatt aacatttcac agtgattgtc attaatacat 240
ttttaaggag tacttcttgt tgattctctt tccacagttt cttacctctg aattatcagc 300
actatgctta tttattctct ttgtctttac tgccttgtaa tccgttacat actttaacat 360
ctatggaaat gtattactga taatcagaat tcagtagaaa ttcttaattg gcttnttact 420
tcacatagca gatntacca cttctcttat tccctacata aaatattagg attattttat 480
gactaatacc atgactcaca gattgagttt gccctctant agggtncata atttctgacc 540
cactagttag attctctgct taccaaaagt canttatgcc tttgcttttt cttcaaaacc 600
ctgnttaatt aggnacggct ttggagataa ttataaaaaa atttcaagct naaantggnt 660
tattattcnt tccnnggttg aaaaaaccca ggaattggca caaannaana aaaagnttat 720
tccnggtttc tttncggnaa aaaaaccaa aaatcttnga aattgttttt taccaaaaaa 780
gacctccnccn gggaaaaagg gngtaaatnt nttccntaaa aacnn 825

```

<210> 77

<211> 904

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ref 9.1
sequence of bacterial artificial chromosome BAC9
using primer C3S11

<220>

<221> modified_base

<222> (1)..(904)

<223> n = g, a, c or t

<400> 77

```

ttcctattca tgaagctaatt cgggatgcaa agaaactatc cacaattcat ggtaaacttc 60
aagaagcatt cagcaaaatt gtatcatcagg taatgattcc aatttctagc ttcactataa 120
agggaaaaaa ctgtctgaaa gcattaatgt tgttttgcac tgatgtcaaa ctagatcccg 180
tgaaatgacc attttaatca gactacaaat gagcgggtcaa aatgatagtt catggccaaa 240
gcaaagctca ttaacaataa aaatgaattc acctaaagta aatgggtgatc atcataaact 300
ttctgcatag cttttttttt ttcatttttg aattattaat taagcaagtt tttaaaaatt 360
gtgattttct gtttcacaag gnaagatcat aagttgngga atctcatttt taaaaaattga 420
taccctattn cttttgctgn ggaaaantgg aagtttttta atattttcaa ggtttttttt 480
aaaattnaaa tggattgttg aaaacctttt aaatnaattt aaaacctacc taaaatantt 540
tttttaatgg nccnngccan ctggaacctt tttatttttt tcccctagga atgggttttac 600
ccaaatccat tcccttttga ataataatct tccctnaatt nccccaaaaa nttttntttt 660
ttttggngng aaaaaatant tggaaaatta aaaaaatggg ggtggggccn taaatgggga 720
ttatttttaa atttcctaaa aaagggantt ttccatttac ctttnaatcc tttttggng 780
gnttcnattt attggggaat cctncncttt tttntncncc ttaaaaaant tagggcctnc 840
caaaatttta aacnttttaa tttttnaaaa nggaaagggn cccctttctt ngcccgggtg 900
gttt 904

```

<210> 78

<211> 681

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Ref 10.1
sequence of bacterial artificial chromosome BAC8
using primer C3S12

<220>
 <221> modified_base
 <222> (1)..(681)
 <223> n = g, a, c or t

<400> 78
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 aaactactcc gttagagaat aaggactttt aatagttaca ataatactct ttcaaactct 180
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 gggtttcttta gaacgtaaaa gcctgaaatc acaccttaaa aacacttcct ttaaccttta 480
 taattttctta attttcacca taaatgattg cgttttatat ttactggggc taactagnat 540
 tttctgntat aggtattctt tccaaccttt ctctattttt tggtactcaa agtgtagtgg 600
 atggaccgga agcattggggg ttcacctggg agaatgggtg gnaatgcaga acccttagac 660
 cccaccccag cccctgtgaa a 681

<210> 79
 <211> 879
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 10.2
 sequence of bacterial artificial chromosome BAC9
 using primer C3S12

<220>
 <221> modified_base
 <222> (1)..(879)
 <223> n = g, a, c or t

<400> 79
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 actactccgt tagagaataa ggacttttaa tagttacaat aatactcttt caaatctttt 180
 atggcagcaa taaaatagta atattgtcta ttttttgaga ctattttcac acatatttta 240
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 taanttnctt aattttcacc cataaaatng attgcngttt tatattttac ctnggggncta 540
 nacctnaggc aatttttctg ggtcataagg gaaatttctt tttcccaaac cttttcttc 600
 ttattttgtt gggncacctc caaaagggtg ntnggtggg gnttngggnc cccngaaaag 660
 gccatttggt ggnttcaccc ccgggggang atttggtttt ggaaaatngt cnnnaaaacc 720
 ttccnnaccc ccnnccccc ggccccntg nnnngaaatc caaaaggatc ttgncnattt 780
 ttttanccaa angancnccc ccnaggngg gatattngtt atttcccaa naangntaa 840
 ggtnnttggc ctttnggggc nttgggtgtt tttntttnn 879

<210> 80
 <211> 786
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 11.1
 sequence of bacterial artificial chromosome BAC9
 using primer HC3AS3

<220>
 <221> modified_base
 <222> (1)..(786)
 <223> n = g, a, c or t

<400> 80
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 tttaatgaac tttatgtata atcaactgaa attaganaaa aaaaagatca atngtaaact 180
 tcatgtaaca ataaaattcc aaacttggat tctaaatgaa nnaaaanant caacctttaa 240
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 taaagggctc aatatgnatg gataaggatg gacatatctt cggactctga gtgggtgtaca 360
 tggcttgatg attgctcact atgtgtgnca ttatggctac ctctctttag gcatgcctgt 420
 taantaggaa gctgaactan caaagnctct tngatgtatn antcctgccg ctnaagaagg 480
 ggncgcntga nncaaagat ttgcnatgtn tctgctatna tngnaagnn tcctngantn 540
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 gngcatctcc cgtanttcac cctcatttna ccntnanttt ataannannn agcccacntn 660
 ncctataggg nactnacgn nttcccnnta ntcantnnna gacaattttt tnnccgcccc 720
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 cttnt 786

<210> 81
 <211> 933
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Ref 12.1
 sequence of bacterial artificial chromosome BAC9
 using primer C3S15

<220>
 <221> modified_base
 <222> (1)..(933)
 <223> n = g, a, c or t

<400> 81
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 tggtttctaa tgttctggta acaagctggt atcttttaag acattttaat gactcaaagg 180
 tacactatac atttaccatt atttatacca tagctaagg taaaaattta ttcactttaa 240
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 agtaatgctt attttaaagg tactattaaa tatgtgaatg tttacactaa tttaccgag 360
 tgggacttca aaatttttat tattgacaat ggctgagaac aattnaaggg tttgactcna 420
 gaactanttc caaacctagc agaataaaaa tcatagatag ccccaaatta atgagtttg 480
 gnaactgtnt caaagttttt ttccattttac atacccaaaa acaggaaatt ttagaatttg 540
 ccngaacctt taccttaaga naaaaaccct tttgtgntna aaaatntant nttaaaattc 600
 cccggggggan taatcttaat nccccgggt gggggccannc nccccnttat aactttggaa 660
 tttaaaaaat cntttttnt ncaaccccaa actgnantng ggtnttttn aaggaaaacc 720
 tttccactng gaagttnnct tttagggnc nancctncna naaannngggg aanattggga 780
 agtcttcccc ttcnttnggg gggngnccca aaaaattctt aataaaaancc ccggggctcc 840
 cattnttagn attttttttt ttggccccac actgtgttna ttaaancccc ncntgctaaa 900
 aatttttnnn gaaaanacct naacccttct nna 933

<210> 82
<211> 100
<212> DNA
<213> Homo sapiens

<220>
<223> exon 60270-20370

<400> 82
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cgcccagaag atcagcaggt aaatatccgg cgtggggcgc 100

<210> 83
<211> 151
<212> DNA
<213> Homo sapiens

<220>
<223> exon 85360-85510

<400> 83
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acaccacagt aagtaacgta ttcaaaatat a 151

<210> 84
<211> 220
<212> DNA
<213> Homo sapiens

<220>
<223> exon 94500-94720

<400> 84
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aatttcctcc agatgatatt gaagttgttt atagtcctcg ggactgcaga actcttgttt 180
cagctgtacc tgaagaaagg taaggagaca ttgacttatt 220

<210> 85
<211> 111
<212> DNA
<213> Homo sapiens

<220>
<223> exon 94870-94980

<400> 85
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<210> 86
<211> 180
<212> DNA
<213> Homo sapiens

<220>
 <223> exon 100110-100290

<400> 86
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<210> 87
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 100340-100600

<400> 87
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 tgcttcccaa ttactttgat cgaactccaa atgaagaaat agaccgtcag aatgatgacc 180
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 agatgtttgc atataaagaa 260

<210> 88
 <211> 141
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 100880-101020

<400> 88
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<210> 89
 <211> 111
 <212> DNA
 <213> Homo sapiens

<220>
 <223> exon 112010-112120

<400> 89
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<210> 90
 <211> 201
 <212> DNA
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<220>
 <223> exon 113680-113880

<400> 90
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gaataatgtt aaatatattt g 201

<210> 91
<211> 140
<212> DNA
<213> Homo sapiens

<220>
<223> exon 115020-115160

<400> 91
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atgcttctca tttccgccac 140

<210> 92
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<223> exon 117200-117410

<400> 92
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<212> DNA
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<220>
<223> exon 123200-12396

<400> 93
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<212> DNA
<213> Homo sapiens

<220>
<223> next part of CLASP starting

<400> 94
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94

<210> 95
<211> 151
<212> DNA
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<220>
<223> exon 5560-5710

<400> 95
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<211> 221
<212> DNA
<213> Homo sapiens

<220>
<223> exon 6680-6900

<400> 96
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<211> 156
<212> DNA
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<220>
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<400> 97
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<210> 98
<211> 2349
<212> DNA
<213> Homo sapiens

<220>
<223> putative promoter region for human CLASP-3,
genomic sequence upstream of human CLASP-3 5'
terminus

<400> 98
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<210> 99

<211> 2008

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-4

<400> 99

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Ser Leu Phe Val Lys Glu Cys Ile Lys Thr Tyr Ser Thr Asp Trp His
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Val Val Asn Tyr Lys Tyr Glu Asp Phe Ser Gly Asp Phe Arg Met Leu
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Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
65                      70          75          80

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225					230					235					240		
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Phe	Ser	Phe	Asp	Ser	Glu	Val	Gln	Arg	Leu	Asp	Phe	Ser	Gly	Ile	Glu		
	275						280					285					
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Asp	Leu	Asn	Pro	Pro	Ser	Val	Arg	Glu	Met	Leu	Trp	Gly	Ser	Ser	Thr		
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Gln	Leu	Ala	Ser	Asp	Gly	Ser	Pro	Lys	Gly	Ser	Ser	Pro	Glu	Ser	Tyr		
	370					375					380						
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Lys	Gln	Val	Cys	Ser	Arg	Leu	Gly	Gln	Tyr	Arg	Met	Pro	Phe	Ala	Trp	450	455	460
Ala	Ala	Arg	Pro	Ile	Phe	Lys	Asp	Thr	Gln	Gly	Ser	Leu	Asp	Leu	Asp	465	470	475
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Lys	Leu	Gln	Ile	Ile	Pro	Gly	Gln	Leu	Asn	Ile	Thr	Val	Glu	Cys	Val	515	520	525
Pro	Val	Asp	Leu	Ser	Asn	Cys	Ile	Thr	Ser	Ser	Tyr	Val	Pro	Leu	Lys	530	535	540
Pro	Phe	Glu	Lys	Asn	Cys	Gln	Asn	Ile	Thr	Val	Glu	Val	Glu	Glu	Phe	545	550	555
Val	Pro	Glu	Met	Thr	Lys	Tyr	Cys	Tyr	Pro	Phe	Thr	Ile	Tyr	Lys	Asn	565	570	575
His	Leu	Tyr	Val	Tyr	Pro	Leu	Gln	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Thr	580	585	590
Phe	Ala	Lys	Ala	Arg	Asn	Ile	Ala	Val	Cys	Val	Glu	Phe	Arg	Asp	Ser	595	600	605
Asp	Glu	Ser	Asp	Ala	Ser	Ala	Leu	Lys	Cys	Ile	Tyr	Gly	Lys	Pro	Ala	610	615	620
Gly	Ser	Val	Phe	Thr	Thr	Asn	Ala	Tyr	Ala	Val	Val	Ser	His	His	Asn	625	630	635
Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Ile	His	645	650	655
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Glu	Ile	Asn	Thr	Lys	Gly	Thr	Thr	Lys	Lys	Gln	Asp	Thr	Val	Glu	Thr	675	680	685
Pro	Val	Gly	Phe	Ala	Trp	Val	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Ile	Ile	690	695	700
Thr	Phe	Glu	Gln	Gln	Leu	Pro	Val	Ser	Ala	Asn	Leu	Pro	Pro	Gly	Tyr	705	710	715
																		720

Leu	Asn	Leu	Asn	Asp	Ala	Glu	Ser	Arg	Arg	Gln	Cys	Asn	Val	Asp	Ile	
				725							730			735		
Lys	Trp	Val	Asp	Gly	Ala	Lys	Pro	Leu	Leu	Lys	Phe	Lys	Ser	His	Leu	
				740							745			750		
Glu	Ser	Thr	Ile	Tyr	Thr	Gln	Asp	Leu	His	Val	His	Lys	Phe	Phe	His	
				755							760			765		
His	Cys	Gln	Leu	Ile	Gln	Ser	Gly	Ser	Lys	Glu	Val	Pro	Gly	Glu	Leu	
				770							775			780		
Ile	Lys	Tyr	Leu	Lys	Cys	Leu	His	Ala	Met	Glu	Ile	Gln	Val	Met	Ile	
				785							790			795		
Gln	Phe	Leu	Pro	Val	Ile	Leu	Met	Gln	Leu	Phe	Arg	Val	Leu	Thr	Asn	
				805							810			815		
Met	Thr	His	Glu	Asp	Asp	Val	Pro	Ile	Asn	Cys	Thr	Met	Val	Leu	Leu	
				820							825			830		
His	Ile	Val	Ser	Lys	Cys	His	Glu	Glu	Gly	Leu	Asp	Ser	Tyr	Leu	Arg	
				835							840			845		
Ser	Phe	Ile	Lys	Tyr	Ser	Phe	Arg	Pro	Glu	Lys	Pro	Ser	Ala	Pro	Gln	
				850							855			860		
Ala	Gln	Leu	Ile	His	Glu	Thr	Leu	Ala	Thr	Thr	Met	Ile	Ala	Ile	Leu	
				865							870			875		
Lys	Gln	Ser	Ala	Asp	Phe	Leu	Ser	Ile	Asn	Lys	Leu	Leu	Lys	Tyr	Ser	
				885							890			895		
Trp	Phe	Phe	Phe	Glu	Ile	Ile	Ala	Lys	Ser	Met	Ala	Thr	Tyr	Leu	Leu	
				900							905			910		
Glu	Glu	Asn	Lys	Ile	Lys	Leu	Pro	Arg	Gly	Gln	Arg	Phe	Pro	Glu	Thr	
				915							920			925		
Tyr	His	His	Val	Leu	His	Ser	Leu	Leu	Leu	Ala	Ile	Ile	Pro	His	Val	
				930							935			940		
Thr	Ile	Arg	Tyr	Ala	Glu	Ile	Pro	Asp	Glu	Ser	Arg	Asn	Val	Asn	Tyr	
				945							950			955		
Ser	Leu	Ala	Ser	Phe	Leu	Lys	Arg	Cys	Leu	Thr	Leu	Met	Asp	Arg	Gly	
				965							970			975		
Phe	Ile	Phe	Asn	Leu	Ile	Asn	Asp	Tyr	Ile	Ser	Gly	Phe	Ser	Pro	Lys	
				980							985			990		
Asp	Pro	Lys	Val	Leu	Ala	Glu	Tyr	Lys	Phe	Glu	Phe	Leu	Gln	Thr	Ile	
				995							1000			1005		
Cys	Asn	His	Glu	His	Tyr	Ile	Pro	Leu	Asn	Leu	Pro	Met	Ala	Phe	Ala	
				1010							1015			1020		
Lys	Pro	Lys	Leu	Gln	Arg	Val	Gln	Asp	Ser	Asn	Leu	Glu	Tyr	Ser	Leu	
				1025							1030			1035		
														1040		

Ser Asp Glu Tyr Cys Lys His His Phe Leu Val Gly Leu Leu Leu Arg
 1045 1050 1055
 Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr Glu Ile Arg Tyr Thr Ala
 1060 1065 1070
 Ile Ser Val Ile Lys Asn Leu Leu Ile Lys His Ala Phe Asp Thr Arg
 1075 1080 1085
 Tyr Gln His Lys Asn Gln Gln Ala Lys Ile Ala Gln Leu Tyr Leu Pro
 1090 1095 1100
 Phe Val Gly Leu Leu Leu Glu Asn Ile Gln Arg Leu Ala Gly Arg Asp
 1105 1110 1115 1120
 Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn Ser Ala Ser Arg Asp Glu
 1125 1130 1135
 Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn Arg Gly Ser Leu Ser Thr
 1140 1145 1150
 Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln Asn Gly His Gly Ile Lys
 1155 1160 1165
 Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro Glu Gly Ala Thr Gly Phe
 1170 1175 1180
 Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr Arg Gln Ser Ser Thr Arg
 1185 1190 1195 1200
 Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp Gln Tyr Glu Ile Arg Ser
 1205 1210 1215
 Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys Met Ile Ser Glu Asp Thr
 1220 1225 1230
 Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile
 1235 1240 1245
 Leu Ile Leu Leu Glu Val Cys Leu Phe His Phe Arg Tyr Met Gly Lys
 1250 1255 1260
 Arg Asn Ile Ala Arg Val His Asp Ala Trp Leu Ser Lys His Phe Gly
 1265 1270 1275 1280
 Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly
 1285 1290 1295
 Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe
 1300 1305 1310
 Thr Leu Asn His Ser Ser Thr Thr Thr Glu Ala Asp Ile Phe His Gln
 1315 1320 1325
 Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu Val Ser Leu Thr Val Leu
 1330 1335 1340
 Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe Lys Thr Gln Leu Leu Asn
 1345 1350 1355 1360

Asn Asp Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Ile His Leu
 1365 1370 1375
 Ala Phe Leu Lys Asn Gly Gln Ser Glu Val Ser Leu Lys His Val Phe
 1380 1385 1390
 Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe Pro Ser Ala Phe Phe Lys
 1395 1400 1405
 Gly Arg Val Asn Met Cys Ala Ala Phe Cys Tyr Glu Val Leu Lys Cys
 1410 1415 1420
 Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn Glu Ala Ser Ala Leu Leu
 1425 1430 1435 1440
 Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr Thr Lys Arg Lys Thr Phe
 1445 1450 1455
 Leu Arg Thr His Leu Gln Ile Ile Ile Ala Val Ser Gln Leu Ile Ala
 1460 1465 1470
 Asp Val Ala Leu Ser Gly Gly Ser Arg Phe Gln Glu Ser Leu Phe Ile
 1475 1480 1485
 Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro Met Lys Ala Thr Ala Phe
 1490 1495 1500
 Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
 1505 1510 1515 1520
 Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Ile
 1525 1530 1535
 Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu
 1540 1545 1550
 Arg Lys Thr Trp Leu Asp Ser Met Ala Lys Ile His Val Lys Asn Gly
 1555 1560 1565
 Asp Phe Ser Glu Ala Ala Met Cys Tyr Val His Val Ala Ala Leu Val
 1570 1575 1580
 Ala Glu Phe Leu His Arg Lys Lys Leu Phe Pro Asn Gly Cys Ser Ala
 1585 1590 1595 1600
 Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu Glu Gly Ala Met Lys Glu
 1605 1610 1615
 Asp Ala Gly Met Met Asp Val His Tyr Ser Glu Glu Val Leu Leu Glu
 1620 1625 1630
 Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu
 1635 1640 1645
 Ile Ile Ser Glu Ile Ser Lys Leu Ile Val Pro Ile Tyr Glu Lys Arg
 1650 1655 1660
 Arg Glu Phe Glu Lys Leu Thr Gln Val Tyr Arg Thr Leu His Gly Ala
 1665 1670 1675 1680

Tyr Thr Lys Ile Leu Glu Val Met His Thr Lys Lys Arg Leu Leu Gly
 1685 1690 1695
 Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu
 1700 1705 1710
 Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser
 1715 1720 1725
 Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr Gly Glu Lys Phe Gly Thr
 1730 1735 1740
 Glu Asn Val Lys Ile Ile Gln Asp Ser Asp Lys Val Asn Ala Lys Glu
 1745 1750 1755 1760
 Leu Asp Pro Lys Tyr Ala His Ile Gln Val Thr Tyr Val Lys Pro Tyr
 1765 1770 1775
 Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn
 1780 1785 1790
 His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly
 1795 1800 1805
 Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu
 1810 1815 1820
 Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn
 1825 1830 1835 1840
 Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Gly Ala Thr Asp Glu
 1845 1850 1855
 Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys Leu Cys Ser Ser Thr Asp
 1860 1865 1870
 Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val
 1875 1880 1885
 Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp
 1890 1895 1900
 Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp
 1905 1910 1915 1920
 Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn
 1925 1930 1935
 Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys
 1940 1945 1950
 Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu
 1955 1960 1965
 Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr
 1970 1975 1980
 Leu His Val Phe Cys Ala Ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr
 1985 1990 1995 2000

Gly Ser Pro Arg Tyr Ala Glu Val
2005

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<211> 2015
<212> PRT
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<220>
<223> human CLASP-5

<400> 100

Met	Thr	His	Leu	Asn	Ser	Leu	Asp	Val	Gln	Leu	Ala	Gln	Glu	Leu	Gly	1	5	10	15
Asp	Phe	Thr	Asp	Asp	Asp	Leu	Asp	Val	Val	Phe	Thr	Pro	Lys	Glu	Cys	20	25	30	
Arg	Thr	Leu	Gln	Pro	Ser	Leu	Pro	Glu	Glu	Gly	Val	Glu	Leu	Asp	Pro	35	40	45	
His	Val	Arg	Asp	Cys	Val	Gln	Thr	Tyr	Ile	Arg	Glu	Trp	Leu	Ile	Val	50	55	60	
Asn	Arg	Lys	Asn	Gln	Gly	Ser	Pro	Glu	Ile	Cys	Gly	Phe	Lys	Lys	Thr	65	70	75	80
Gly	Ser	Arg	Lys	Asp	Phe	His	Lys	Thr	Leu	Pro	Lys	Gln	Thr	Phe	Glu	85	90	95	
Ser	Glu	Thr	Leu	Glu	Cys	Ser	Glu	Pro	Ala	Ala	Gln	Ala	Gly	Pro	Arg	100	105	110	
His	Leu	Asn	Val	Leu	Cys	Asp	Val	Ser	Gly	Lys	Gly	Pro	Val	Thr	Ala	115	120	125	
Cys	Asp	Phe	Asp	Leu	Arg	Ser	Leu	Gln	Pro	Asp	Lys	Arg	Leu	Glu	Asn	130	135	140	
Leu	Leu	Gln	Gln	Val	Ser	Ala	Glu	Asp	Phe	Glu	Lys	Gln	Asn	Glu	Glu	145	150	155	160
Ala	Arg	Arg	Thr	Asn	Arg	Gln	Ala	Glu	Leu	Phe	Ala	Leu	Tyr	Pro	Ser	165	170	175	
Val	Asp	Glu	Glu	Asp	Ala	Val	Glu	Ile	Arg	Pro	Val	Pro	Glu	Cys	Pro	180	185	190	
Lys	Glu	His	Leu	Gly	Asn	Arg	Ile	Leu	Val	Lys	Leu	Leu	Thr	Leu	Lys	195	200	205	
Phe	Glu	Ile	Glu	Ile	Glu	Pro	Leu	Phe	Ala	Ser	Ile	Ala	Leu	Tyr	Asp	210	215	220	
Val	Lys	Glu	Arg	Lys	Lys	Ile	Ser	Glu	Asn	Phe	His	Cys	Asp	Leu	Asn	225	230	235	240
Ser	Asp	Gln	Phe	Lys	Gly	Phe	Leu	Arg	Ala	His	Thr	Pro	Ser	Val	Ala	245	250	255	

Ala Ser Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser
 260 265 270
 Ser Asp Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly
 275 280 285
 Asp Ile Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp
 290 295 300
 Gly Gly Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu
 305 310 315 320
 Ser Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala
 325 330 335
 Pro Ile Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu
 340 345 350
 Val Thr Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg
 355 360 365
 Arg Thr Leu Ala Gln Ser Arg Arg Leu Ser Glu Arg Ala Leu Ser Leu
 370 375 380
 Glu Glu Asn Gly Val Gly Ser Asn Phe Lys Thr Ser Thr Leu Ser Val
 385 390 395 400
 Ser Ser Phe Phe Lys Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu
 405 410 415
 Phe Lys Phe Leu Ala Asp Tyr Lys Arg Ser Ser Ser Leu Gln Arg Arg
 420 425 430
 Val Lys Ser Ile Pro Gly Leu Leu Arg Leu Glu Ile Ser Thr Ala Pro
 435 440 445
 Glu Ile Ile Asn Cys Cys Leu Thr Pro Glu Met Leu Pro Val Lys Pro
 450 455 460
 Phe Pro Glu Asn Arg Thr Arg Pro His Lys Glu Ile Leu Glu Phe Pro
 465 470 475 480
 Thr Arg Glu Val Tyr Val Pro His Thr Val Tyr Arg Asn Leu Leu Tyr
 485 490 495
 Val Tyr Pro Gln Arg Leu Asn Phe Val Asn Lys Leu Ala Ser Ala Arg
 500 505 510
 Asn Ile Thr Ile Lys Ile Gln Phe Met Cys Gly Glu Asp Ala Ser Asn
 515 520 525
 Ala Met Pro Val Ile Phe Gly Lys Ser Ser Gly Pro Glu Phe Leu Gln
 530 535 540
 Glu Val Tyr Thr Ala Val Thr Tyr His Asn Lys Ser Pro Asp Phe Tyr
 545 550 555 560
 Glu Glu Val Lys Ile Lys Leu Pro Ala Lys Leu Thr Val Asn His His
 565 570 575

Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala	
			580					585					590			
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn	
		595					600					605				
Glu	Arg	Leu	Gln	Thr	Gly	Ser	Tyr	Cys	Leu	Pro	Val	Ala	Leu	Glu	Lys	
	610					615					620					
Leu	Pro	Pro	Asn	Tyr	Ser	Met	His	Ser	Ala	Glu	Lys	Val	Pro	Leu	Gln	
625					630					635					640	
Asn	Pro	Pro	Ile	Lys	Trp	Ala	Glu	Gly	His	Lys	Gly	Val	Phe	Asn	Ile	
			645						650					655		
Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu	
			660					665					670			
Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro	
	675						680					685				
Ile	Arg	Val	Leu	Asp	Gln	Lys	Ile	Ser	Glu	Met	Ala	Leu	Glu	His	Glu	
	690					695					700					
Leu	Lys	Leu	Ser	Ile	Ile	Cys	Leu	Asn	Ser	Ser	Arg	Leu	Glu	Pro	Leu	
705					710					715					720	
Val	Leu	Phe	Leu	His	Leu	Val	Leu	Asp	Lys	Leu	Phe	Gln	Leu	Ser	Val	
				725					730					735		
Gln	Pro	Met	Val	Ile	Ala	Gly	Gln	Thr	Ala	Asn	Phe	Ser	Gln	Phe	Ala	
			740					745					750			
Phe	Glu	Ser	Val	Val	Ala	Ile	Ala	Asn	Ser	Leu	His	Asn	Ser	Lys	Asp	
		755					760					765				
Leu	Ser	Lys	Asp	Gln	His	Gly	Arg	Asn	Cys	Leu	Leu	Ala	Ser	Tyr	Val	
	770					775					780					
His	Tyr	Val	Phe	Arg	Leu	Pro	Glu	Val	Gln	Arg	Asp	Val	Pro	Lys	Ser	
785					790					795					800	
Gly	Ala	Pro	Thr	Ala	Leu	Leu	Asp	Pro	Arg	Ser	Tyr	His	Thr	Tyr	Gly	
				805					810					815		
Arg	Thr	Ser	Ala	Ala	Ala	Val	Ser	Ser	Lys	Leu	Leu	Gln	Ala	Arg	Val	
			820					825					830			
Met	Ser	Ser	Ser	Asn	Pro	Asp	Leu	Ala	Gly	Thr	His	Ser	Ala	Ala	Asp	
	835						840					845				
Glu	Glu	Val	Lys	Asn	Ile	Met	Ser	Ser	Lys	Ile	Ala	Asp	Arg	Asn	Cys	
	850					855					860					
Ser	Arg	Met	Ser	Tyr	Tyr	Cys	Ser	Gly	Ser	Ser	Asp	Ala	Pro	Ser	Ser	
865					870					875					880	
Pro	Ala	Ala	Pro	Arg	Pro	Ala	Ser	Lys	Lys	His	Phe	His	Glu	Glu	Leu	
				885					890					895		

Ala Leu Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln
 900 905 910
 His Val His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe
 915 920 925
 Ser Asp Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr
 930 935 940
 Ser Glu Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln
 945 950 955 960
 Ala Glu Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu
 965 970 975
 Ser Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys
 980 985 990
 Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met
 995 1000 1005
 Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn
 1010 1015 1020
 Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys
 1025 1030 1035 1040
 Pro Ser Ile Ser Ser Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp
 1045 1050 1055
 Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln
 1060 1065 1070
 His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp
 1075 1080 1085
 Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala
 1090 1095 1100
 Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys
 1105 1110 1115 1120
 Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly
 1125 1130 1135
 Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp
 1140 1145 1150
 Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala
 1155 1160 1165
 Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe
 1170 1175 1180
 Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln
 1185 1190 1195 1200
 Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe
 1205 1210 1215

Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
 1220 1225 1230
 Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
 1235 1240 1245
 Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
 1250 1255 1260
 Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
 1265 1270 1275 1280
 Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
 1285 1290 1295
 Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
 1300 1305 1310
 Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
 1315 1320 1325
 Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn
 1330 1335 1340
 Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile
 1345 1350 1355 1360
 Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly
 1365 1370 1375
 Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr
 1380 1385 1390
 Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe
 1395 1400 1405
 Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys
 1410 1415 1420
 His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser
 1425 1430 1435 1440
 Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala
 1445 1450 1455
 Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala
 1460 1465 1470
 Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg
 1475 1480 1485
 Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln
 1490 1495 1500
 Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn
 1505 1510 1515 1520
 Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro
 1525 1530 1535

Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala
 1540 1545 1550
 Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His
 1555 1560 1565
 Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala
 1570 1575 1580
 Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr
 1585 1590 1595 1600
 Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu
 1605 1610 1615
 Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly
 1620 1625 1630
 Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
 1635 1640 1645
 Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val
 1650 1655 1660
 Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
 1665 1670 1675 1680
 Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
 1685 1690 1695
 Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
 1700 1705 1710
 Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
 1715 1720 1725
 Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
 1730 1735 1740
 Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
 1745 1750 1755 1760
 Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
 1765 1770 1775
 Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu
 1780 1785 1790
 Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg
 1795 1800 1805
 Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu
 1810 1815 1820
 Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala
 1825 1830 1835 1840
 Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe
 1845 1850 1855

Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr
 1860 1865 1870
 Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met
 1875 1880 1885
 Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly
 1890 1895 1900
 Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro
 1905 1910 1915 1920
 Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe
 1925 1930 1935
 Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr
 1940 1945 1950
 Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys
 1955 1960 1965
 Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu
 1970 1975 1980
 Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His
 1985 1990 1995 2000
 Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
 2005 2010 2015

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<220>
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 Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr
 35 40 45
 Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu
 50 55 60
 Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile
 65 70 75 80
 Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys
 85 90 95
 Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His
 100 105 110

Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu
 435 440 445
 Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro
 450 455 460
 Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu
 465 470 475 480
 Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser
 485 490 495
 Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp
 500 505 510
 Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu
 515 520 525
 Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu
 530 535 540
 Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr
 545 550 555 560
 Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg
 565 570 575
 Gln Gly Ser Ala Arg Asn Ile Thr Val Lys Val Gln Phe Met Tyr Gly
 580 585 590
 Glu Asp Pro Ser Asn Ala Met Pro Val Ile Phe Gly Lys Ser Ser Cys
 595 600 605
 Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala Val Val Tyr His Asn Arg
 610 615 620
 Ser Pro Asp Phe His Glu Glu Ile Lys Val Lys Leu Pro Ala Thr Leu
 625 630 635 640
 Thr Asp His His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys Gln
 645 650 655
 Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro Val Gly Tyr Thr Trp Ile
 660 665 670
 Pro Met Leu Gln Asn Gly Arg Leu Lys Thr Gly Gln Phe Cys Leu Pro
 675 680 685
 Val Ser Leu Glu Lys Pro Pro Gln Ala Tyr Ser Val Leu Ser Pro Glu
 690 695 700
 Val Pro Leu Pro Gly Met Lys Trp Val Asp Asn His Lys Gly Val Phe
 705 710 715 720
 Asn Val Glu Val Val Ala Val Ser Ser Ile His Thr Gln Asp Pro Tyr
 725 730 735
 Leu Asp Lys Phe Phe Ala Leu Val Asn Ala Leu Asp Glu His Leu Phe
 740 745 750

Pro Val Arg Ile Gly Asp Met Arg Ile Met Glu Asn Asn Leu Glu Asn
 755 760 765
 Glu Leu Lys Ser Ser Ile Ser Ala Leu Asn Ser Ser Gln Leu Glu Pro
 770 775 780
 Val Val Arg Phe Leu His Leu Leu Leu Asp Lys Leu Ile Leu Leu Val
 785 790 795 800
 Ile Arg Pro Pro Val Ile Ala Gly Gln Ile Val Asn Leu Gly Gln Ala
 805 810 815
 Ser Phe Glu Ala Met Ala Ser Ile Ile Asn Arg Leu His Lys Asn Leu
 820 825 830
 Glu Gly Asn His Asp Gln His Gly Arg Asn Ser Leu Leu Ala Ser Tyr
 835 840 845
 Ile His Tyr Val Phe Arg Leu Pro Asn Thr Tyr Pro Asn Ser Ser Ser
 850 855 860
 Pro Gly Pro Gly Gly Leu Gly Gly Ser Val His Tyr Ala Thr Met Ala
 865 870 875 880
 Arg Ser Ala Val Arg Pro Ala Ser Leu Asn Leu Asn Arg Ser Arg Ser
 885 890 895
 Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly Thr Pro Thr Ser Pro Asp
 900 905 910
 Asp Glu Val Arg Ser Ile Ile Gly Ser Lys Gly Leu Asp Arg Ser Asn
 915 920 925
 Ser Trp Val Asn Thr Gly Gly Pro Lys Ala Ala Pro Trp Gly Ser Asn
 930 935 940
 Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn
 945 950 955 960
 Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr
 965 970 975
 Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln
 980 985 990
 Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala
 995 1000 1005
 Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr
 1010 1015 1020
 Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg
 1025 1030 1035 1040
 Phe Met Asp Asp Ile Ala Ala Leu Val Ser Thr Ile Ala Ser Asp Ile
 1045 1050 1055
 Val Ser Arg Phe Gln Lys Asp Thr Glu Met Val Glu Arg Leu Asn Thr
 1060 1065 1070

Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly
 1075 1080 1085
 Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys
 1090 1095 1100
 Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp
 1105 1110 1115 1120
 Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu
 1125 1130 1135
 Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Ser Val Ser
 1140 1145 1150
 Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln
 1155 1160 1165
 Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His
 1170 1175 1180
 Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro
 1185 1190 1195 1200
 Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val
 1205 1210 1215
 His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro
 1220 1225 1230
 Gln Ile Lys Ala Arg Val Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile
 1235 1240 1245
 Ile Met Glu Thr Val Pro Gln Leu Tyr Asp Phe Thr Glu Thr His Asn
 1250 1255 1260
 Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu
 1265 1270 1275 1280
 Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr
 1285 1290 1295
 Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr
 1300 1305 1310
 Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu
 1315 1320 1325
 Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu
 1330 1335 1340
 Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
 1345 1350 1355 1360
 Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
 1365 1370 1375
 Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
 1380 1385 1390

Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
 1395 1400 1405
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
 1410 1415 1420
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
 1425 1430 1435 1440
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
 1445 1450 1455
 Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
 1460 1465 1470
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
 1475 1480 1485
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
 1490 1495 1500
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
 1505 1510 1515 1520
 Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
 1525 1530 1535
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys
 1540 1545 1550
 Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr
 1555 1560 1565
 Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val
 1570 1575 1580
 Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
 1585 1590 1595 1600
 Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr
 1605 1610 1615
 Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln
 1620 1625 1630
 Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val
 1635 1640 1645
 Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met
 1650 1655 1660
 Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp
 1665 1670 1675 1680
 Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu
 1685 1690 1695
 Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu
 1700 1705 1710

Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe
 1715 1720 1725
 Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp
 1730 1735 1740
 Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr
 1745 1750 1755 1760
 Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser
 1765 1770 1775
 Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile
 1780 1785 1790
 Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His
 1795 1800 1805
 Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly
 1810 1815 1820
 Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr
 1825 1830 1835 1840
 Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala
 1845 1850 1855
 Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly
 1860 1865 1870
 Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
 1875 1880 1885
 Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
 1890 1895 1900
 Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
 1905 1910 1915 1920
 Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
 1925 1930 1935
 Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
 1940 1945 1950
 Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
 1955 1960 1965
 Arg Val Asn Val Thr His Lys Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
 1970 1975 1980
 Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala
 1985 1990 1995 2000
 Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln
 2005 2010 2015
 Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln
 2020 2025 2030

Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His
 2035 2040 2045
 Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp
 2050 2055 2060
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 2065 2070 2075 2080
 Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro
 2085 2090

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 <211> 1980
 <212> PRT
 <213> Homo sapiens

 <220>
 <223> human CLASP-2

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 Gln Gly Arg Tyr Ile Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu
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 Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp
 35 40 45
 Trp His Leu Val Asn Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg
 50 55 60
 Gln Leu Pro Asn Lys Val Val Lys Leu Asp Lys Leu Pro Val His Val
 65 70 75 80
 Tyr Glu Val Asp Glu Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu
 85 90 95
 Gly Ser Gln Lys Gly Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly
 100 105 110
 Asn Met Asn Ser Ala Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg
 115 120 125
 Phe Phe His Leu Ile Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe
 130 135 140
 Tyr Lys Asp Glu Lys Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu
 145 150 155 160
 Asp Ser Cys Met Gly Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala
 165 170 175
 Phe Glu Leu Lys Met Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp
 180 185 190
 Ser Glu Val Glu Met Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu
 195 200 205

Gln Leu Asn Phe Glu Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser
 210 215 220
 His Glu Asp Asp Glu Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu
 225 230 235 240
 Asp Ser Tyr Leu Pro Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile
 245 250 255
 Lys Leu Lys Ser Glu Ser Arg Val Lys Leu Phe Tyr Leu Asp Pro Asp
 260 265 270
 Ala Gln Lys Leu Asp Phe Ser Ser Ala Glu Pro Glu Val Lys Ser Phe
 275 280 285
 Glu Glu Lys Phe Gly Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser
 290 295 300
 Phe Asn Leu Gln Cys Cys Val Ala Glu Asn Glu Glu Gly Pro Thr Thr
 305 310 315 320
 Asn Val Glu Pro Phe Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr
 325 330 335
 Asn Arg Lys Ile Ser Ala Asp Phe His Val Asp Leu Asn His Phe Ser
 340 345 350
 Val Arg Glu Met Leu Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser
 355 360 365
 Gly Gln Ser Pro Ser Val Leu Lys Gly Ile Leu His Glu Ala Ala Met
 370 375 380
 Gln Tyr Pro Lys Gln Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp
 385 390 395 400
 Ile Phe Leu Val Ala Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr
 405 410 415
 His Cys Ala Glu Pro Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala
 420 425 430
 Gln Lys Val Leu Lys Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln
 435 440 445
 Tyr Arg Met Pro Phe Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala
 450 455 460
 Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln
 465 470 475 480
 Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp
 485 490 495
 Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn
 500 505 510
 Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val
 515 520 525

Asn	Ser	Ser	Tyr	Ile	Pro	Thr	Lys	Gln	Phe	Glu	Thr	Cys	Ser	Lys	Thr	530	535	540
Pro	Ile	Thr	Phe	Glu	Val	Glu	Glu	Phe	Val	Pro	Cys	Ile	Pro	Lys	His	545	550	555
Thr	Gln	Pro	Tyr	Thr	Ile	Tyr	Thr	Asn	His	Leu	Tyr	Val	Tyr	Pro	Lys	565	570	575
Tyr	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Ser	Phe	Ala	Lys	Ala	Arg	Asn	Ile	580	585	590
Ala	Ile	Cys	Ile	Glu	Phe	Lys	Asp	Ser	Asp	Glu	Glu	Asp	Ser	Gln	Pro	595	600	605
Leu	Lys	Cys	Ile	Tyr	Gly	Arg	Pro	Gly	Gly	Pro	Val	Phe	Thr	Arg	Ser	610	615	620
Ala	Phe	Ala	Ala	Val	Leu	His	His	His	Gln	Asn	Pro	Glu	Phe	Tyr	Asp	625	630	635
Glu	Ile	Lys	Ile	Glu	Leu	Pro	Thr	Gln	Leu	His	Glu	Lys	His	His	Leu	645	650	655
Leu	Leu	Thr	Phe	Phe	His	Val	Ser	Cys	Asp	Asn	Ser	Ser	Lys	Gly	Ser	660	665	670
Thr	Lys	Lys	Arg	Asp	Val	Val	Glu	Thr	Gln	Val	Gly	Tyr	Ser	Trp	Leu	675	680	685
Pro	Leu	Leu	Lys	Asp	Gly	Arg	Val	Val	Thr	Ser	Glu	Gln	His	Ile	Pro	690	695	700
Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	His	Leu	Gly	Tyr	Gln	Glu	Leu	Gly	705	710	715
Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys	725	730	735
Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln	740	745	750
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser	755	760	765
Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu	770	775	780
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu	785	790	795
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala	805	810	815
Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu	820	825	830
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys	835	840	845

Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu	850	855	860	
Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr	865	870	875	880
Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile	885	890	895	
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu	900	905	910	
Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val	915	920	925	
Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro	930	935	940	
Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg	945	950	955	960
Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn	965	970	975	
Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr	980	985	990	
Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro	995	1000	1005	
Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln	1010	1015	1020	
Asp	Leu	Gln	Leu	Asp	Tyr	Ser	Leu	Thr	Asp	Glu	Phe	Cys	Arg	Asn	His	1025	1030	1035	1040
Phe	Leu	Val	Gly	Leu	Leu	Leu	Arg	Glu	Val	Gly	Thr	Ala	Leu	Gln	Glu	1045	1050	1055	
Phe	Arg	Glu	Val	Arg	Leu	Ile	Ala	Ile	Ser	Val	Leu	Lys	Asn	Leu	Leu	1060	1065	1070	
Ile	Lys	His	Ser	Phe	Asp	Asp	Arg	Tyr	Ala	Ser	Arg	Ser	His	Gln	Ala	1075	1080	1085	
Arg	Ile	Ala	Thr	Leu	Tyr	Leu	Pro	Leu	Phe	Gly	Leu	Leu	Ile	Glu	Asn	1090	1095	1100	
Val	Gln	Arg	Ile	Asn	Val	Arg	Asp	Val	Ser	Pro	Phe	Pro	Val	Asn	Ala	1105	1110	1115	1120
Gly	Met	Thr	Val	Lys	Asp	Glu	Ser	Leu	Ala	Leu	Pro	Ala	Val	Asn	Pro	1125	1130	1135	
Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His	Lys	1140	1145	1150	
Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr	Ser	1155	1160	1165	

Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu
 1170 1175 1180
 Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys
 1185 1190 1195 1200
 Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser
 1205 1210 1215
 Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu
 1220 1225 1230
 Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe
 1235 1240 1245
 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
 1250 1255 1260
 Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr
 1265 1270 1275 1280
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
 1285 1290 1295
 Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
 1300 1305 1310
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
 1315 1320 1325
 Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu
 1330 1335 1340
 Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser
 1345 1350 1355 1360
 Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His
 1365 1370 1375
 Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln
 1380 1385 1390
 Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg
 1395 1400 1405
 Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp
 1410 1415 1420
 Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys
 1425 1430 1435 1440
 Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met
 1445 1450 1455
 Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His
 1460 1465 1470
 Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly
 1475 1480 1485

Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys
 1490 1495 1500
 Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val
 1505 1510 1515 1520
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
 1525 1530 1535
 Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
 1540 1545 1550
 Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp
 1555 1560 1565
 Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu
 1570 1575 1580
 Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu
 1585 1590 1595 1600
 Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
 1605 1610 1615
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
 1620 1625 1630
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
 1635 1640 1645
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp
 1650 1655 1660
 Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe
 1665 1670 1675 1680
 Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr
 1685 1690 1695
 Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys
 1700 1705 1710
 Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn
 1715 1720 1725
 Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val
 1730 1735 1740
 Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe
 1745 1750 1755 1760
 Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr
 1765 1770 1775
 Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg
 1780 1785 1790
 Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile
 1795 1800 1805

Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala
 1810 1815 1820
 Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser
 1825 1830 1835 1840
 Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
 1845 1850 1855
 Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe
 1860 1865 1870
 Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu
 1875 1880 1885
 Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu
 1890 1895 1900
 Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu
 1905 1910 1915 1920
 Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile
 1925 1930 1935
 Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro
 1940 1945 1950
 Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr
 1955 1960 1965
 Met Val His Gly Met Thr Ser Ser Ser Ser Val Val
 1970 1975 1980

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 <212> PRT
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<220>
 <223> human CLASP-7

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 Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val Pro Leu Thr
 35 40 45
 Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro
 50 55 60
 Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala
 65 70 75 80
 Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu
 85 90 95

Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala
 100 105 110
 Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln
 115 120 125
 Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu
 130 135 140
 Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly
 145 150 155 160
 Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser
 165 170 175
 Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser Ser Ile Phe
 180 185 190
 Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser Leu Leu Glu
 195 200 205
 Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr Leu Arg Arg
 210 215 220
 Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala Pro Asp Glu
 225 230 235 240
 Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro Arg Glu His
 245 250 255
 Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys Phe Glu Ile
 260 265 270
 Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp Val Arg Glu
 275 280 285
 Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser
 290 295 300
 Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr
 305 310 315 320
 Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser Pro Asp Ile
 325 330 335
 Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser
 340 345 350
 Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys
 355 360 365
 Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys
 370 375 380
 Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His
 385 390 395 400
 Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg Asp Ser Asp
 405 410 415

Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly
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 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly
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 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala
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 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg
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 Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
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 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
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 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
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 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
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 His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
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 625 630 635 640
 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
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 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe
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 Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu
 675 680 685
 Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys
 690 695 700
 Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln
 705 710 715 720
 Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu
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Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn
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 Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser
 755 760 765
 Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val
 770 775 780
 Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu
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 His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala
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 1875 1880 1885
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 1905 1910 1915 1920
 Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly Ser Val
 1925 1930 1935
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 1955 1960 1965
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 1970 1975 1980
 Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His Arg Glu
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 Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln
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 Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser
 65 70 75 80
 Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His
 85 90 95
 Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser
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 Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile
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 Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His
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 Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr
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 165 170 175
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 Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly
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Ser	Ala	Asp	Phe	His	Val	Asp	Leu	Asn	His	Ala	Ala	Val	Arg	Gln	Met	
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Tyr	Ala	Gln	Lys	Ile	Leu	Lys	Ser	Asn	Arg	Gln	Phe	Cys	Ser	Lys	Leu	
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 565 570 575
 Arg Gln Glu Ser Ser Lys Ile Ser Thr Glu Asp Leu Val Lys Leu Val
 580 585 590
 Ser Asp Tyr Arg Arg Ala Asp Arg Ile Ser Lys Met Gln Thr Ile Pro
 595 600 605
 Gly Ser Leu Asp Ile Ala Val Asp Asn Val Pro Leu Glu His Pro Asn
 610 615 620
 Cys Val Thr Ser Ser Phe Ile Pro Val Lys Pro Phe Asn Met Met Ala
 625 630 635 640
 Gln Thr Glu Pro Thr Val Glu Val Glu Glu Phe Val Tyr Asp Ser Thr
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 Lys Tyr Cys Arg Pro Tyr Arg Val Tyr Lys Asn Gln Ile Tyr Ile Tyr
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 Pro Lys His Leu Lys Tyr Asp Ser Gln Lys Cys Phe Asn Lys Ala Arg
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 850 855 860
 Glu Lys Asp Met Ser Gln Ser Pro Thr Ser Asn Phe Ile Arg Ser Cys
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Lys Asn Leu Leu Asn Val Glu Lys Ile His Ala Ile Met Ser Phe Leu
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 Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys
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 Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp
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 Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr
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 Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu
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 Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro
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 Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu
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Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys
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Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp
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Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser
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Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys
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Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His
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Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly
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Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr
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 1890 1895 1900
 Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
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 1955 1960 1965
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 Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser
 1985 1990 1995 2000
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 immunoreceptor tyrosine-based activation motif
 (ITAM) motif 1
 <220>
 <221> MOD_RES
 <222> (1)..(11)
 <223> Xaa = any amino acid
 <400> 128
 Tyr Xaa Xaa Val Xaa Xaa Xaa Tyr Xaa Xaa Leu
 1 5 10

<210> 129
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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immunoreceptor tyrosine-based activation motif
(ITAM) motif 2

<220>
<221> MOD_RES
<222> (1)..(10)
<223> Xaa = any amino acid

<400> 129
Tyr Xaa Xaa Val Xaa Xaa Tyr Xaa Xaa Lys
1 5 10

<210> 130
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CLASP-3
immunoreceptor tyrosine-based activation motif
(ITAM) motif 3

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<221> MOD_RES
<222> (1)..(13)
<223> Xaa = any amino acid

<400> 130
Tyr Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Thr
1 5 10

<210> 131
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly
conserved non-tyrosine containing region from
motif E

<220>
<221> MOD_RES
<222> (2)
<223> Xaa = conservative amino acid substitution, Xaa =
Ile or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Xaa = any amino acid

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<220>
<221> MOD_RES
<222> (7)
<223> Xaa = conservative amino acid substitution, Xaa =
      Asp, Glu or Gln

<220>
<221> MOD_RES
<222> (8)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (9)
<223> Xaa = conservative amino acid substitution, Xaa =
      Met, Ile, Leu or Val

<400> 131
Pro Xaa Glu Xaa Ala Ile Xaa Xaa Xaa
  1                      5

<210> 132
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:highly
      conserved non-tyrosine containing region from
      motif F

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<223> Xaa = any amino acid

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<222> (3)
<223> Xaa = Met or Leu

<220>
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<222> (6)
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      Gln or Asn

<220>
<221> MOD_RES
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<223> Xaa = any amino acid

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<220>
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 <222> (9)
 <223> Xaa = Val or Ile

 <220>
 <221> MOD_RES
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 <223> Xaa = any amino acid

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 <222> (15)
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 <400> 132
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 1 5 10 15

<210> 133
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:antisense oligo
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<400> 133
 ctattactaa ggcttcgaga acgattta 28

<210> 134
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:antisense oligo
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<400> 134
 ctggaaaacg acttttcctt ggagcctcaa g 31

<210> 135
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:antisense oligo
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<400> 135
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<400> 140
gacccattag gaggtctac

19

<210> 141
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
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primer HC4AS3'

<400> 141
cgggatccat tgtcaccgta catctgc

27

<210> 142
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sense primer
hC1S5'

<400> 142
tatgtctcag tcacctacct g

21

<210> 143
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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primer HClAS3'Kpn

<400> 143
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30

<210> 144
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:sense primer
C1S7

<400> 144
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20

<210> 145
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<212> DNA
<213> Artificial Sequence

Q11
A13

<220>
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used for human CLASP-3 5' RACE

<400> 145
aaaaacatct tgggaaggat aagtgatag

29

<210> 146
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
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used for human CLASP-3 5' RACE

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28

<210> 147
<211> 29
<212> DNA
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<220>
<223> Description of Artificial Sequence:HC3RACE7 primer
used for human CLASP-3 5' RACE

<400> 147
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29

<210> 148
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:HC3RACE8 primer
used for human CLASP-3 5' RACE

<400> 148
ttcacttgaa gcacgtccgg agttaggc

28



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